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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Wed May 1 16:48:49 1996, MasPar time 42.82 Seconds 622.612 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-462-355-1 (1-1446) from US08462355.seq 1446 Description:

Perfect Score:

1 ATGCCTCTTTCTCTGCTGA......AAAGAAATAGTACAACTGTG 1446
TACCGCAGAAAGAGACGACT......TTTCTTTATCATGTTGACAC N.A. Sequence:

Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD:

30947 seqs, 9219370 bases x 2 Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

n-issued 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 8.992; Variance 4.572; scale 1.967

Statistics:

SUMMARIES

		ю					
Result No.	Score	Query Match	Query Match Length DB	DB	αı	Description	Pred. No.
1	40	2.8		6	PCT-US93-1	Sequence 39, Applicati	1.58e-12
7	38	5.6		6	PCT-US93-1	Sequence 41,	3.48e - 11
3	34	2.4	720	6	PCT-US93-1	Sequence 35,	1.47e - 08
4	32	2.2		10	PCT-US94-1	Sequence 7,	•
5	32	2.2		10	PCT-US94-1	Sequence 1,	
9	32	2.2		10	PCT-US94-1	Sequence 3,	2.78e-07
7	29	2.0		6	PCT-US93-1	Sequence 3,	2.03e-05
œ	78	1.9		10	PCT-US94-1	Sequence 16, Applicati	00
6	56	1.8		4	US-07-816-	ຕ້	1.26e - 03
c 10	24	1.7	105	4	US-07-865-	Sequence 13, Applicati	1.75e-02

11 24 1.7 1307 11 PCT-US95-0 Sequence 1, Application 25 1.7 1317 9 PCT-US93-1 Sequence 45, Application 14 24 1.7 1351 4 US-07-816- Sequence 5, Application 15 25 1.7 1737 4 US-08-102- Sequence 5, Application 15 25 1.7 1737 4 US-08-102- Sequence 5, Application 16 25 1.7 1737 4 US-08-102- Sequence 5, Application 17 17 15 1.6 1634 4 US-07-816- Sequence 1, Application 18 23 1.6 1734 4 US-07-816- Sequence 1, Application 19 23 1.6 1734 4 US-07-816- Sequence 1, Application 19 22 1.5 15 15 18 10 PCT-US94-0 Sequence 2, Application 22 1.5 15 15 18 10 PCT-US92-0 Sequence 5, Application 24 1.5 1106 8 PCT-US92-0 Sequence 5, Application 24 1.5 1106 11 PCT-US93-0 Sequence 6, Application 25 11 1.5 1106 11 PCT-US93-0 Sequence 7, Application 26 22 1.5 1200 8 PCT-US93-0 Sequence 7, Application 27 115 1106 11 PCT-US93-0 Sequence 7, Application 28 11 1.5 1206 4 US-07-816- Sequence 7, Application 29 11 1.5 1206 4 US-07-816- Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1.5 1200 8 PCT-US93-0 Sequence 7, Application 20 11 1 12 12 12 12 12 12 12 12 12 12 12 1	tio 1.75e-02 ati 4.75e-03	4.		tio 4.75e-03	tio 4.75e-03	ati 6.30e-02	tio 6.30e-02	ati 6.30e-02	ati 2.20e-01	۲;	_	tio 7.42e-01	ati 7.42e-01	tio 7.42e-01	tio 2.20e-01	tio 2.20e-01	tio 7.42e-01	?	۲.	tio 7.42e-01	tio 7.42e-01	ati 7.42e-01	٦ ،	i 7	tio 7.42e-01	tio 7.42e-01	~	2.4	tio 2.42e+00	tio 2.42e+00	7	7		ati 2.42e+00
11 24 1.7 1307 11 12 25 1.7 1317 9 14 24 1.7 1317 9 15 25 1.7 1372 4 16 25 1.7 1737 4 18 23 1.6 1634 4 20 22 1.5 1106 4 20 22 1.5 1106 11 21 22 1.5 1106 11 22 21 1.5 1106 11 23 21 1.5 1106 11 24 21 1.5 1106 11 25 22 1.5 1106 11 26 22 1.5 1106 11 29 22 1.5 1206 4 30 21 1.5 1200 1 33 21 1.5 1200	1, A	, ,	2,	4,	2,	13,	-	11,	22,	5,	4,	'n,	31,	2,	1,	1,	۲,	9,	4,	ω,	2,	43,	۲,	27,	Ξ,	-i	Ŋ,	. ,	'n	5,	5,	1,	15,	15,
11 24 1.7 1307 12 25 1.7 1317 13 25 1.7 1317 16 25 1.7 1371 16 25 1.7 1371 17 17 1572 18 23 1.6 1634 20 22 1.5 1652 21 22 1.5 1662 23 21 1.5 1166 24 21 1.5 1166 25 21 1.5 1161 26 22 1.5 1206 27 21 1.5 1161 28 21 1.5 1161 29 22 1.5 1206 30 22 1.5 1206 31 21 1.5 124 32 21 1.5 124 33 21 1.5 133 34	PCT-US95-0 PCT-US93-1	US-07-816-	US-08-041-	US-08-202-	PCT-US94-0	US-07-865-	US-07-816-	US-07-816-	PCT-US94-0	PCT-US92-0	PCT-US95-0	PCT-US92-0	PCT-US93-1	PCT-US95-0	PCT-US95-0	PCT-US92-0	US-07-816-	US-07-816-	us-07-759-	US-08-202-	US-08-202-	PCT-US93-1	PCT-US94-0	PCT-US93-1	PCT-US93-0	US-07-882-	PCT-US92-0	PCT-US95-0	PCT-US92-0	PCT-US92-0	PCT-US92-0	PCT-US94-0	US-08-046-	PCT-US93-1
200 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1307 11	1351 4	1572 4			-	-	-									1244 4	1296 4	1510 3	1748 4	1883 4	1901 9						П				1		~1
111 112 113 113 114 115 116 117 117 117 117 117 117 117 117 117	1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
	24 25	25	24	52	52	23	23	23	22	22	21	21	21	21	22	22	21	22	21	21	21	21	21	21	21	21	20	20	20	70	20	70	70	20
	11	13	14	15	16	17	18	19	•	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	4	4	4	43	4	c 45

ALI GNMENTS

Sequence 39, Application PC/TUS9311153.
Sequence 39, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 JT 1 PCT-US93-11153-39 STANDARD; DNA; UNC; 1872 BP. MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: NUMBER OF SEQUENCES: ZIP: 60606 01-JAN-1900 XXXXXX

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0; Gaps Query Match 2.6%; Score 38; DB 9; Length 2098; Best Local Similarity 61.0%; Pred. No. 3.48e-11; Matches 105; Conservative 0; Mismatches 67; Indels Sequence 2098 BP; 371 A; 594 C; 671 G; 462 T; 0 other; SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/11153 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452 REFERENCE/DOCKET NUMBER: 31794 TELEPHONE: (312) 474-6300
TELEX: (312) 474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single REGISTRATION NUMBER: 35,302 TELECOMMUNICATION INFORMATION: MOLECULE TYPE: DNA (genomic) FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION: NAME: Noland, Greta E. NAME/KEY: CDS LOCATION: 551..1681 TOPOLOGY: linear FILING DATE: FEATURE:

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D PCT-US93-11153-35 STANDARD; DNA; UNC; 720 BP.

AC xxxxx
DT 01-JAN-1900
DE Sequence 35, Application PC/TUS9311153.
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweitart, Vicki L.
CC TITLE OF INVENTION: Ovvel Seven Transmembrane Receptors
CC MUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago

May 1 16:4

TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 17

ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston

STATE: Texas COUNTRY: USA ZIP: 77210

CORRESPONDENCE ADDRESS:

PCT-US94-10358-1 STANDARD; DNA; UNC; 1618

Sequence 1, Application PC/TUS9410358. Sequence 1, Application PC/TUS9410358 GENERAL INFORMATION:

01-JAN-1900

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APPLICANT:

COMPUTER READBLE FORM:
MEDUH YPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25

APPLICATION NUMBER: PCT/US94/10358 FILING DATE: Concurrently herewith

PRIOR APPLICATION DATA:

CLASSIFICATION:

CURRENT APPLICATION DATA:

ö Gaps .; 0 Query Match 2.2%; Score 32; DB 10; Length 1610; Best Local Similarity 83.3%; Pred. No. 2.78e-07; Matches 40; Conservative 0; Mismatches 8; Indels Qy 1139 TGGTGGTGGTGTCTTTCTTGTCTGCTGGACTCCATACCACATT 1186 Db 1092 TGGTGGTGGTGGTGTTCATCGTCTGCTGGACTCCCATTCACATTT 1139 MOLECULE TYPE: CDNA Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other; COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATEMINI RELEASE #1.0, VERSION #1.25
SNERRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358 NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37, 259
REFERENCE/DOCKET NUMBER: INDA005P—
TELECOMMUNICATION INFORMATION:
TELECHONE: (512) 418-3000
TELEFAX: (713) 789-2679 FILING DATE: Concurrently herewith FILING DATE: 13 SEPTEMBER 1993 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/120.601 TELEX: 79-0924 INFORMATION FOR SEQ ID NO: 7: MEDIUM TYPE: Floppy disk LENGTH: 1610 base pairs SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear CLASSIFICATION: 888888888888888888888888888888

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à g ð 음 à 663 CATCTTCACCAGCATATTCACCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTGT 722 603 GGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCAATAGATTACTACAA 662 TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS Gaps .**.** Score 32; DB 10; Length 1618; Pred. No. 2.78e-07; 0; Mismatches 49; Indels Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other; MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATEMTIM RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA: PCT-US94-10358-3 STANDARD; DNA; UNC; 1618 BP. NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--APPLICATION NUMBER: PCT/US94/10358 FILING DATE: Concurrently herewith ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston STATE: Texas Sequence 3, Application PC/TUS9410358.
Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT: APPLICATION NUMBER: 08/120.601 FILING DATE: 13 SEPTEMBER 1993 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679 LENGTH: 1618 base pairs Query Match 2.2%; Best Local Similarity 62.3%; Matches 81; Conservative TYPE: nucleic acid STRANDEDNESS: single CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: NAME/KEY: CDS LOCATION: 214..1410 NUMBER OF SEQUENCES: MOLECULE TYPE: cDNA TOPOLOGY: linear TELEX: 79-0924 723 CCACCCAGTC 732 375 CAAGCCAATC 384 COUNTRY: USA ZIP: 77210 01-JAN-1900 XXXXXX RESULT g g 8888888888888888888888 셤 à ð ð

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603 GGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCAATAGATTACTACAA 662 663 CATGIICACCAGCAIAIICACCCICTGCACCAIGAGCGIGGACCGCIACAITGCIGICG 722 0; Gaps IIILE OF INVENTION: Novel Seven Transmembrane Receptors Query Match 2.2%; Score 32; DB 10; Length 1618; Best Local Similarity 62.3%; Pred. No. 2.78e-07; Matches 81; Conservative 0; Mismatches 49; Indels ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: 6300 Sears Tower, 233 South Wacker Drive Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other; .T 7 PCT-US93-11153-3 STANDARD; DNA; UNC; 120 BP. Sequence 3, Application PC/TUS9311153.
Sequence 3, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
APPLICANT: Schweikart, Vicki L. REFERENCE/DOCKET NUMBER: INDA005P-TELECOMMUNICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION: COMPUTER: IBM PC compatible NAME: WILSON, MARK B. REGISTRATION NUMBER: 37,259 TELEX: 79-0924 INFORMATION FOR SEQ ID NO: 3: TELEPHONE: (512) 418-3000 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELEFAX: (713) 789-2679 SEQUENCE CHARACTERISTICS: LENGTH: 1618 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear CORRESPONDENCE ADDRESS: LOCATION: 339..1235 NUMBER OF SEQUENCES: MOLECULE TYPE: CDNA CITY: Chicago STATE: Illinois COUNTRY: USA NAME/KEY: CDS 375 CAAGCCAATC 384 723 CCACCCAGTC 732 ZIP: 60606 01-JAN-1900 XXXXX RESULT

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COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: US/07/816,283 APPLICATION NUMBER: 08/120.601 FILING DATE: 13 SEPTEMBER 1993 ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARK B. REGISTRATION NUMBER: 37,259 Sequence 3, Application US/07816283.
Sequence 3, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Seino, Susumu TELEX: 79-0924 INFORMATION FOR SEQ ID NO: 16: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679 NAME: McDaniel, C. Steven ITTORNEY/AGENT INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 1567 base pairs NUMBER OF SEQUENCES: 12 FILING DATE: 19911231 TYPE: nucleic acid STRANDEDNESS: single PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: LOCATION: 173..1273 CLASSIFICATION: 435 TOPOLOGY: linear MOLECULE TYPE: cDNA NAME/KEY: CDS 01-JAN-1900 XXXXXX RESULT Q O ; 0 TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 17 256 GGACAGTGGCCCTACGCCAGGTTCCTATGCAAGCTCATCCCTCCATCATTGTCCTCAAC 315 22 GGACTGTGGAGGACGGCTCCTTCCTGTGCAAAGGGAGCTCCTACATGATCTCCGTCAAT 81 0; Mismatches 33; Indels 0; Gaps Query Match 2.0%; Score 29; DB 9; Length 120; Best Local Similarity 65.3%; Pred. No. 2.03e-05; Matches 62; Conservative 0; Mismatches 33; Indels MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: Sequence 120 BP; 26 A; 30 C; 32 G; 32 T; 0 other; PCT-US94-10358-16 STANDARD; DNA; UNC; 1567 BP 82 ATGCACTGCAGTGTCCTCCTGCTCACTTGCATGAG 116 APPLICATION NUMBER: PCT/US94/10358 APPLICATION NUMBER: PCT/US93/11153 FILING DATE: Concurrently herewith APPLICATION NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION: ADDRESSEE: Arnold, White & Durkee Sequence 16, Application PC/TUS9410358.
Sequence 16, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT: OPERATING SYSTEM: PC-DOS/MS-DOS REFERENCE/DOCKET NUMBER: 31794 TELECOMMUNICATION INFORMATION:
TELEPRONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS: NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302 MOLECULE TYPE: DNA (genomic) LENGTH: 120 base pairs CURRENT APPLICATION DATA: STREET: P. 0. Box 4433 PRIOR APPLICATION DATA: STRANDEDNESS: single COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS: TYPE: nucleic acid TOPOLOGY: linear CLASSIFICATION: CITY: Houston STATE: Texas COUNTRY: USA ZIP: 77210 FILING DATE

ö Query Match 1.9%; Score 28; DB 10; Length 1567; Best Local Similarity 79.2%; Pred. No. 8.21e-05; Matches 38; Conservative 0; Mismatches 10; Indels 1 Vy 1128 TCGAGTGCCGTGCTGCTGTTTTTTTTTTCTCTGCTGCTCT 1175 949 TCGACTGCTGCTAGTGGTGGCTGTTTTGTGGGCTGCTGGACGC 996 Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 other; REFERENCE/DOCKET NUMBER: INDA005P--TELECOMMUNICATION: 88888888888888888888888888888888

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US-07-816-283-3 STANDARD; DNA; UNC; 1265 BP

01-JAN-1900

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g ð FITLE OF INVENTION: SOMATOSTATIN RECEPTORS ADDRESSEE: Arnold, White & Durkee STREET: PO Box 4433 CITY: Houston STATE: Texas

SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

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TITLE OF INVENTION: Restriction Fragment Length TITLE OF INVENTION: Polymorphism Test For Haplotyping Domesticated Fow 451 CACTGGCCCTTCGGCGCGCTACTTTGCCGCCTGGTGCTCAGCGTGGATGCGGTCAACATG 510 511 ITCACCAGCATCTACTGTCTGACTGTGCTTAGTGTGGACCGCTATGTGGCTGTGGTGCAC 570 Gaps .; 0 Query Match 1.8%; Score 26; DB 4; Length 1265; Best Local Similarity 60.3%; Pred. No. 1.26e-03; 0; Mismatches 50; Indels MOLECULE TYPE: cDNA Sequence 1265 BP; 229 A; 379 C; 366 G; 291 T; 0 other; MEDIUM TYPE: 3M Double Density 5 1/4" diskette US-07-865-662F-13 STANDARD; DNA; UNC; 105 BP. OPERATING SYSTEM: MS DOS Version 3.20 APPLICATION NUMBER: US/07/865, 662F FILING DATE: 07 April, 1992 CLASSIFICATION: 435 COUNTRY: United States of America ZIP: 91010-0269 Sequence 13, Application US/0786562F. Sequence 13, Application US/0786562F Patent No. 5451670 APPLICATION NUMBER: 07/688,326 FILING DATE: 22 April 1991 APPLICATION NUMBER: 07/588,922 FILING DATE: 27 September 1990 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double TELECOMMUNICATION INFORMATION: APPLICANT: Marcia M. Miller TELEPHONE: 713-787-1400 TELEFAX: 713-789-2679 CURRENT APPLICATION DATA: PRIOR APPLICATION DATA: 76; Conservative COMPUTER READABLE FORM: SOFTWARE: Microsoft COMPUTER: Wang PC STATE: California TOPOLOGY: linear GENERAL INFORMATION: CITY: Duarte 571 CCGATC 576 11 111 379 CCAATC 384 01-JAN-1900 XXXXX Matches 88888888888888 Q à 셤 à õ

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298 AGGGGATGAGCTTGCATAGGAACCTGCCGTAGGGCCACTGTCCCTGGAGAGCCAAGTGAG 239 3 VKVGNNAKNSNNNKSNNAVKNGNNAKNSGKNKSANAVNNGNNA-KNSNNNKSNNMCTRDN 61 1; Gaps TITLE OF INVENTION: DNA ENCODING BRADYKININ B1 RECEPTOR 34; Mismatches 51; Indels 1.7%; Score 24; DB 4; Length 105; 9.5%; Pred. No. 1.75e-02; SOFTWARE: PatentIn Release #1.0, Version #1.25 IMMEDIATE SOURCE: Synthetically Prepared Sequence 105 BP; 15 A; 0 C; 8 G; 1 T; 81 other; 238 CCAGCGAGAAGGCCAAGGAGGAGGAGG 204 62 KNNRNAAKNINSGVADNKNNASNNYDNGSGVADNK 96 ORIGINAL SOURCE: Synthetically Prepared REFERENCE/DOCKET NUMBER: No. 5451670e TELECOMMUNICATION INFORMATION: LT 11 PCT-US95-04464-1 STANDARD; DNA; UNC; 1307 FILING DATE: 9 December 1987 APPLICATION NUMBER: US 07/068,176 FILING DATE: 23 June 1988 APPLICATION NUMBER: US 07/130,529 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 1, Application PC/TUS9504464 Sequence 1, Application PC/TUS9504464 GENERAL INFORMATION: 07/210,405 ADDRESSEE: John W. Wallen III STREET: P.O. Box 2000 CITY: Rahway STATE: New Jersey APPLICANT: Bierillo, Kathleen K. APPLICANT: Borkowski, Joseph A. APPLICANT: Linemeyer, David L. APPLICANT: Menke, John G. APPLICANT: Hess, John F. REGISTRATION NUMBER: 16,541 TELEX: No. 5451670e INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: FILING DATE: 30 June 1987 ATTORNEY/AGENT INFORMATION: TELEPHONE: (202) 783-6040 TELEFAX: (202) 783-6031 MEDIUM TYPE: Floppy disk NAME: Irons, Edward S. TYPE: Nucleic Acid STRANDEDNESS: Double Best Local Similarity 9.5%; 9; Conservative CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: NUMBER OF SEQUENCES: TOPOLOGY: Linear MOLECULE TYPE: DNA COUNTRY: USA 105 ZIP: 07065 TELEFAX: LENGTH: xxxxxx 01-JAN-1900 Query Match Matches 음 g a å

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                                                                                                                                                                                                                                                                                                                                                                                                       974 GTGGTTGCCTTCCTGGTCTGCTGGGCCCCTTACCACTTCTTTGCCTTCCTGGAATT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 1147 GTGGCTGTCTTTTTTTTTCTGCTGGACTCCATACCACATTTGGGGAGTCCTGTCATT 1202
                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Novel Seven Transmembrane Receptors NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                    Query Match 1.7%; Score 24; DB 11; Length 1307; Best Local Similarity 71.4%; Pred. No. 1.75e-02;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
Sequence 1307 BP; 282 A; 400 C; 306 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-11153-45 STANDARD; DNA; UNC; 1317 BP
               APPLICATION NUMBER: PCT/US95/04464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Application PC/TUS9311153. Sequence 45, Application PC/TUS9311153 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 REFERENCE/DOCKET NUMBER: 19202 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                  REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,302
                                                                                                                                                                TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                 TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
                                                                                  NAME: Wallen III, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-NOV-1992
                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Noland, Greta E.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         40; Conservative
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: USA
                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606
                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1900
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXX
                                                                                                                                                                                                                                                                                                                                                                         Matches
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ö 452 GGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAA 511 255 GGGACAGTGGCCCTACGCCAGGTTCCTATGCAAGCTCATCCCTCCATCATGTCCTCAA 314 0; Caps Query Match 1.7%; Score 25; DB 9; Length 1317; Best Local Similarity 61.7%; Pred. No. 4.75e-03; 0; Mismatches 41; Indels 512 CCTCTACAGCAGTGCTCTCATCCTGGCCTTCATCAGTCTGGACCGCT 558 Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T; 0 other; US-08-462-355-1 mi REFERENCE/DOCKET NUMBER: 31794 TELECOMMUNICATION INFORMATION TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 45: TELEPHONE: (312) 474-6300 SEQUENCE CHARACTERISTICS: LENGTH: 1317 base pairs TYPE: nucleic acid STRANDEDNESS: single (312) 474-0448 NAME/KEY: CDS LOCATION: 201..1211 66; Conservative TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE: TELEFAX: Query Match May 1 16:41 Matches 88888888888888888888 Q D δ g δ

SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: Sequence 5, Application US/07816283.
Sequence 5, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS US-07-816-283-5 STANDARD; DNA; UNC; 1351 BP ADDRESSEE: Arnold, White & Durkee APPLICATION NUMBER: US/07/816,283 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: STREET: PO Box 4433 CITY: Houston COUNTRY: USA STATE: Texas ZIP: 77210 01-JAN-1900 XXXXXX RESULT

FELECOMMUNICATION INFORMATION:

TELEPHONE: 713-787-1400

TELEFAX: 713-789-2679

NAME: McDaniel, C. Steven

ATTORNEY/AGENT INFORMATION:

FILING DATE: 19911231

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 5:

79-0924

SEQUENCE CHARACTERISTICS:

LENGTH: 1351 base pairs

TYPE: NUCLEIC ACID STRANDEDNESS: double

8888888888

TOPOLOGY: linear

US-08-462-355-1 mi

US-08-041-219A-5 STANDARD; DNA; UNC; 1572 BP.

01-JAN-1900

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1168 TGGACTCCATACCACAT 1184

887 IGGCTICCCTICIACAI 903

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Sequence 5, Application US/08041219A. Sequence 5, Application US/08041219A Patent No. 5427922 GENERAL INFORMATION:

APPLICANT: KURODA, Shun'ichi

APPLICANT: FUJISAWA, Yukio

APPLICANT: KONISHI, HISOAKA
TITLE OF INVENTION: ANGIOTENSIN II TYPE-1 RECEPTOR AND ITS
TITLE OF INVENTION: PRODUCTION
WOMBER OF SEQUENCES:
CORRESPONDENCE ANDERSS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM:

ZIP: 20036

CITY: Washington

STATE: D.C. COUNTRY: U.S.A.

APPLICATION NUMBER: US/08/041,219A FILING DATE: 31-MAR-1993 CLASSIFICATION: 435

APPLICATION NUMBER: JP 085445-1992 FILING DATE: 07-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 101393-1992 FILING DATE: 21-APR-1992 APPLICATION NUMBER: JP 027835-1993

PRIOR APPLICATION DATA:

RIOR APPLICATION DATA:

FILING DATE: 17-FEB-1993 ATTORNEY/AGENT INFORMATION: NAME: Mueller, Douglas P.

.**;**

Score 25; DB 4; Length 1351; Pred. No. 4.75e-03; 0; Mismatches 26; Indels

Query Match 1.7%; Best Local Similarity 66.2%; Matches 51; Conservative

MOLECULE TYPE: CDNA Sequence 1351 BP; 307 A; 375 C; 333 G; 336 T; 0 other;

ö 262 TGGCCCTACGCCAGGTTCCTATGCAAGCTCATCCCCTCCATCATTGTCCTCAACATGTTT 321 0; Gaps IIILE OF INVENTION: Antibodies to Human IL-8 Type B Receptor Query Match 1.7%; Score 24; DB 4; Length 1572; Best Local Similarity 62.2%; Pred. No. 1.75e-02; Matches 61; Conservative 0; Mismatches 37; Indels TISSUE TYPE: Placental Sequence 1572 BP; 424 A; 359 C; 329 G; 460 T; 0 other; ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk 579 GCTAGTGTTCCTACTCACGTGTCTCAGCATTGATCG 616 322 GGCAGTGTCTTCCTGCTTACTGCCATTAGCCTGGATCG 359 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS REGISTRATION NUMBER: 30,300 SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,056

FILING DATE: 25-FEB-1994

APPLICATION NUMBER: 07/677211

PRIOR APPLICATION DATA:

CLASSIFICATION: 436

FILING DATE: 29-MAR-1991

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TOPOLOCY: linear Sequence 1737 Bp; 454 A; 411 C; 373 G; 499 T; 0 other; ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single 88888888888888888

Query Match 1.7%; Score 25; DB 4; Length 1737; Best Local Similarity 61.7%; Pred. No. 4.75e-03; Matches 66; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

255 GGGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCGTCCTCAA 314 387 GGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAA 446 ò

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Search completed: Wed May 1 16:49:35 1996 Job time: 46 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

Wed May 1 16:38:24 1996, MasPar time 589.87 Seconds 881.274 Million cell updates/sec Run on:

Tabular output not generated.

(1-1446) from US08462355.seq >US-08-462-355-1 Description: Perfect Score: Title:

1 ATGCCGTCTTTCTCTGCTGA......AAAGAAATAGTACAACTGTG 1446 TACCGCAGAAAGAGACGACT......TTTCTTTATCATGTTGACAC N.A. Sequence: сошр:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD:

518261 seqs, 179750453 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST9 10:EST91 11:EST12 13:EST13 14:EST14 15:EST91 14:EST14 15:EST91 14:EST14 20:EST92 21:EST92 23:EST92 24:EST92 25:EST92 24:EST92 25:EST92 23:EST92 24:EST93 23:EST93 24:EST93 23:EST93 24:EST93 23:EST93 24:EST93 23:EST93 24:EST94 25:EST95 26:EST96 27:EST93 23:EST93 24:EST94 25:EST95 25:EST95 26:EST96 27:EST94 24:EST94 25:EST96 27:EST94 25:EST96 27:EST93 27:EST93 27:EST93 27:EST93 27:EST93 27:EST94 27:EST94 27:EST94 27:EST94 27:EST94 27:EST94 27:EST94 27:EST94 27:EST96 27:E

EST-STS-TWO

Database:

110:enEST2 111:enEST3 112:enEST4 113:enEST5 114:enEST6 115:enEST7 116:enEST8 117:enEST9 118:enEST10 119:enEST11 120:enEST12 121:enEST13 122:enEST14 123:enEST15 121:enEST17 126:enEST18 127:enEST19 95:qnEST1 96:qnEST2 97:qnEST3 98:qnEST4 99:qnEST5 100:qnEST6 101:qnEST7 102:qnEST8 103:qnEST9 104:qnEST10 105:qnEST11 106:qnSTS1 107:qnSTS2 108:qnSTS3 109:enEST1

US-08-462-355-1 rst May 1 1640 128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

scale 6.028 Variance 1.885; Mean 11.364; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match	>	Query Match Length	DB	OI.	Description	Pred. No.
- !	: i					- 1
421 29.1		484	22	88	7505	0.00e+00
ä		471	9	R92269	yq06g01.rl Homo sapie	0.00e+00
		471	116	HS269192	yq06g01.rl Homo sapie	0.00e+00
		256	98	T91438	ye01d06.rl Homo sapie	
246 17.0		319	75	T49050	Ношо	0.00e+00
212 14.7		334	34	R01558	rl Homo	0.00e+00
83 5.7		297	20	R58715	omo sapie	3.31e-125
68 4.7		349	35	R06476	rl Homo say	9.09e-92
31 2.1		466		R15256	rl Homo sapi	.03e-
		183	26	R81583	rl Homo sapi	.31e-1
		238	m	M78084	2 Homo sapien	.32e-1
6 1.		497		T90501	sl Homo	.70e-1
1:		249	12	H29103	Homo	6.35e-07
3 1.		198		H14008	Homo sapien	'n.
3 1		205	٢	H14012	EST00038 Homo sapiens	5e-0
23 1.6		232	27	HSC2UF111	par	٠:
23 1.6		355	101	H75904	08f03.rl	٦.
3 1.		355	125	HS 904230	Ношо	i.
3 1,		388		T53360		=
23 1.6		421	٠.	HS 609197	1 Homo	
		421	62	R98609		1.55e-05
23 1.6		431	-	G09547	human STS CHLC.GCT7D1	.55e-0
23 1.6		452		R82424	Нопо	1.55e-05
23 1.6		475	-	R31127	Нопо	ĸ.
23 1.6		508		н87900	Нопс	÷
3 1.		508		HS900247	1 Homo	
2 1.		203		R93324	Homo s	3.3
22 1.5		203	٦	HS324189	1 Homo sa	3.33e-04
2 1.		222	7	HSC2JF042	parti	3.33e-04
ij		254	7	HSC2JG042	H. sapiens partial cD	3.33e-04
2 1.		270	23	HSC35C062		3.33e-04
2 1.		299		T24084	seq2272 Homo sapiens	3.33e-04
1.		301		RS5001	EST107661 Rattus sp.	ڧ
22 1.5		316		HS04115		
2 1.		316	_	T33041		3.33e-04
2 1.		324		T02691	0047M7 Plasmodium fal	3.33e - 04
2 1		324		PF691		
		347		R30721		
		352		HS148G05B	Human fetal brain	3.339-04
		35.5		2000 T T MILL A B C 0 5 B	fatal brain c	
		365	, –	T66281	iccar prain	; :
		200	0	3 5	rl Domo capi	330-0
22 1.3		445	4	103650	raniens	
		1 10	7	•	HOHO GET	339
22 1.3		516	2 6	1950	int Homo sapi	3 5
7.7		-	3	0	rozosi nomo sapi	Š

ALI GNMENTS

07-JUN-1995 EST mRNA 484 bp R77881 RESULT LOCUS

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May 1 16:40

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DEFINITION	yi77h05.rl Homo sapiens cDNA clone 145305 5' similar to SP:BLR1 HUMAN P32302 BURKITT'S LYMPHOMA RECEPTOR ;.	Db 181 cctqttacagcttcattgtcttccgaatgcaaagggccgcttcgccaagtctcagagca
ACCESS ION KEYWORDS	R77881 EST.	
SOURCE	human clone=145305 library-Soares placenta NbZHP vector=p77730 (Pharmacia) with a modified polylinker host=0H10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a local primer All resistant of the strand cDNA was primed with a	Db 241 aaacctttcgagtggccgtggtggtggtggctgtcttcttgtctgctggactccatacc
	NOT 1 = 0.1190(UI) PLIME: () AACTGGAAGATTCGCGCCCGCGCAGAATTTTTTTTTTTT	Db 301 acattttgggggtcctgttcattgcttactgacccagaaactcccttggggaaaaactc
ORGANISM		Db 361 tgatgttctggggatcangtatgcattgctctagcatctgccaattagttgctttaatcc
	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE AUTHORS	<pre>1 (bases i to 484) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and</pre>	<pre>Qy 1296 CITCCITIAIGCCCTCITGGGGAAGGAITIIAGGGAAGGAAGGAAGGCAAGGC</pre>
TITLE JOURNAL	Wilson, R. The WashU-Merck EST Project Unpublished (1995)	SULT 2
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 251 Source: IMAGE Consortium, Lial. This clone is available royalty-free through LIAL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	LOCUS R92269 471 bp mRNA EST 25-AUG-1 DEFINITION yq06q01.rl Homo sapiens CDNA clone 196176 5'. ACCESSION R92269 KEYWORDS EST. SOURCE human clone=196176 library=Soares fetal liver spleen INFLS (ampicillin resistant) primer=M13RP1 Rsite=1=Pac Liver and spleen from a 20 week-post conception male fetus strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATRAATATAAAGATCTTTTTTTTTTTTTTT
FEATURES source	NCBI gi: 852991 Location/Qualifiers 1484 /organism="Homo sapiens" /clone="145305"	vector. Library went through one round of normalization. CONSTRUCTED by Bento Soares and M.Fatima Bonaldo. ORCANISM Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deutarostomia; Chordata; Vertebrata; Gnathostomata; Osteic Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; The
BASE COUNT ORIGIN	107 a	Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo REFERENCE 1 (bases 1 to 471) AUTHORS Hillier,L., Clark, U. Obbuque,T., Elliston,K., Hawkins,M., Hawkins,M., Hawkins,M., Clark,M., M., Clark,M., Clar
Query Match Best Local : Matches 4	Query Match 29.1%; Score 421; DB 55; Length 484; Best Local Similarity 96.9%; Pred. No. 0.00e+00; Matches 469; Conservative 0; Mismatches 8; Indels 7; Gaps 7;	noumenter, nutumenter, nucess, r., Legin, Legin, Legin, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. at Wilson, R., Whenck EST Project
Db 1 1 Qy 881 7	<pre>1 taaagctgtccctagcgctctagcaattccttctacgagtctgagctaccacaaggtt 60 11 </pre>	T.
Db 61 :	tccaggattattacaatttaggccaattcacagatgacgatcaagtgccaacaccctcg 120 	Mashington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fee: 314 206 1801
Db 121 9	121 tggcaataacgatcactaggctaqtggtggtttcctgctgccctctgttatcatgatag 180 	Email: est@watcon.wustl.edu High quality sequence stops: 341 Source: IMAGE Consortium, LIAL

uterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, rcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, stor=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
apicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI ver and spleen from a 20 week-post conception male fetus. 1st tttgggagtcctgttcattgcttactgacccagaaactcccttggggaaaactc 360 lman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
rsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
evaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and 25-AUG-1995 nan clone=196176 library=Soares fetal liver spleen INFLS cheria; Archonta; Primates; Catarrhini; Hominidae; Homo. llier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., caryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; 2269 471 bp mRNA EST 06g01.rl Homo sapiens cDNA clone 196176 5', 2269 e WashU-Merck EST Project published (1995) ntact: Wilson RK shU-Merck EST Project (bases 1 to 471) no sapiens lson, R. 1359 482

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

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US-08-462-355-1 rst

School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estëwatson.wustl.edu High quality sequence stops: 341 Source: IMAGE Consortium, LINL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further

Contact: Wilson RK WashU-Merck EST Project Washington University

information. NCBI gi: 959809

Location/Qualifiers

source

/organism="Homo sapiens'

/clone="196176"

/note="human"

BP; 123 A; 115 C; 88 <1..>471 mRNA

G; 137 T; 8 other; Sequence 471

4;

Gaps

4;

3; Indels

0; Mismatches

384; Conservative

Matches

윤 ð 셤 8

Best Local Similarity

Query Match

Length 471;

Score 358; DB 60; Pred. No. 0.00e+00;

24.8%; 98.2%;

8 others

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137

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88

115 c

æ

123

COUNT

BASE CO

<1..>471

/organism="Homo sapiens" /clone="196176" /note="human"

Location/Qualifiers

NCBI gi:

1..471 959809

Bource

FEATURES

557 19 aaatgaatgataggttagateetteetettteeaaacaaatgateateettggaeagtee 120

ctgctaggttaacaagtcaaaatctgtattctaatgtatttaaacctgctgatgtggtct CTGCTAGGTTAACAAGTCAAAATCTGTATTCTAATGTATTTAAACCTGCTGATGTGGTCT

ccactgtcttccaacctcaaacatttcaaagaccttctgcagattcactccctaggggtt

121 677

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180

240 196 300 856

Gaps 4; Length 471; Indels ä Score 358; DB 116; Pred. No. 0.00e+00; 0; Mismatches tch 24.8%; al Similarity 98.2%; 384; Conservative Local Similarity Query Match Matches Best

4;

8 1 acttttatggagatccactagaaaacaggtctcttgaaaacattgttcagccgcctggag 셤

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919 δ 121 ccactgrottccaacctcaaacattccaagaccttctgcagattcactccctaggggt 180 g

677 CCACTGTCTTCCAACCTCCAAACATTTCAAAGACCTTCTGCAGATTCACTCCCTAGGGGTT 736 ð 181 ctgctaggttaacaagtcaaaatctgtattctaatgtatttaaacctgctgatgtggtct 240 셤

5 241 g

797

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ctgatgcttttctctctactncatttaaagctgttccctagcgcttctagcaattccttc 360

301 857

g

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8

CACCTAAAATCCCCCAGTGGGTTTCCTATTGAAGATCACGAAACCAGCCCACTGGATAACT

301 857 g δ

361 tacggagtcttgaggttaccacaaggtttnc 391 g

TACG-AGTCT-GAGCT-ACCACAAGGTTTCC 943 916

ð

22-MAR-1995 ye01d06.rl Homo sapiens cDNA clone 116459 5' T91438 4 DEFINITION ACCESSION KEYWORDS RESULT LOCUS

EST

strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 human clone=116459 library=Soares fetal liver spleen lNFLS
vector=pT7f3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st

vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo SOURCE

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The WashU-Merck EST Project";

Unpublished

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae

Version 1)

yq06g01.rl Homo sapiens cDNA clone 196176 5'

Homo sapiens (human)

1-471

28-AUG-1995 (Rel. 45, Created) 28-AUG-1995 (Rel. 45, Last updated,

standard; RNA; EST; 471

HS269192

R92269;

US-08-462-355-1 rst

71 tecaaacaaatgateateettggacagteeceaetgtetteeaaeeteaaaattteaaa 130 131 gaccttctgcagattcactccctaggggttctgctaggttaacaagtcaaaatctgtatt 190 707 GACCITCTGCAGAITCACTCCCTAGGGGTTCTGCTAGGTTAACAAGTCAAAAICTGTAIT 766 251 tgaagatcacggaaaccagcccactgg 277 -GAAGATCACG-AAACCAGCCCACTGG 850 264; Conservative Best Local Similarity Query Match 9 source ORGANISM BASE COUNT 826 TITLE JOURNAL Matches REFERENCE AUTHORS FEATURES RESULT ORIGIN g ð 셤 ŏ 음 ð g à g ð Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; ï Source: IMAGE Consortium, LIML This clone is available royalty-free through LIML; contact the 1063 TGTTACAGCTTCATTGTCTTCCGAATGCAAAGGGGCGCGCTTCGCCAAGTCTCAGAGAA 1122 !MAGE Consortium (info@image.llnl.gov) for further information. 121 gcaataacgatcactaggctagtggtggtttcctgctgccctctgttatcatgatagcc 180 181 tgttacagcttcattgtcttccgaatgcaaaggggccgcttcgccaagtctcagagcaaa 240 8 08-FEB-1995 Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 256)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Gaps 1 agetgttccctagcgcttctagcaattccttctacgagtctgagctaccacaaggtttcc 4444 Forest Parkway, Box 8501, St. Louis, MO 63108 Ξ human clone=70592 library=Stratagene placenta (#937225) Length 256; 1 others 1; Indels yb08e05.rl Homo sapiens cDNA clone 70592 5'. 149050 Washington University School of Medicine Score 248; DB 86; Pred. No. 0.00e+00; 0; Mismatches 69 /organism="Homo sapiens"/clone="116459" High quality sequence stops: 216 Location/Qualifiers 56 g The WashU-Merck EST Project Email: est@watson.wustl.edu WashU-Merck EST Project /note="human" Query Match 17.2%; Best Local Similarity 99.2%; 1123 ACCTTCGAGTGGCCG 1138 70 c 254; Conservative 241 acctttcgagtngccg 256 Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 1..256 NCBI gi: 723351 æ Wilson, R. 9 ഗ source DEFINITION ORGANISM BASE COUNT Matches REFERENCE AUTHORS JOURNAL ACCESS ION KEYWORDS FEATURES TITLE SOURCE RESULT ORIGIN LOCUS 셤 à 셤 쇰 ð g 셤 ð ð δ

3;

Gaps

3

Indels

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0; Mismatches

17.0%; Score 246; DB 75; Length 319; 98.9%; Pred. No. 0.00e+00;

vector=pBluescript SK- host=SOIR cells (kanamycin resistant) primer=M13RP1 Rsite1=EcoR1 Rsite2=Xho1 Placental tissue from a Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGCCACGAG-3'; 3' adaptor sequence: Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; This clone is available royalty-free through LLML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. l (bases 1 to 319)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eutheria; Primates; Catarrhini; Hominidae; Homo. Washington University School of Medicine 66 /organism="Homo sapiens" High qality sequence stops: 268 Source: IMAGE Consortium, LLNL 5'-crccagttttttttttttt-3' Location/Qualifiers Б Email: est@watson.wustl.edu 55 WashU-Merck EST Project Other_ESTs: yb08e05.s1 /clone="70592 /note="human 20 80 08 Unpublished (1995) Contact: Wilson RK Fax: 314 286 1810 Tel: 314 286 1800 1.,319NCBI gi: 650910 Homo sapiens 82

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S	10B s.RI 1st nnded th Pac th Pac th PT3	mmalia;	_		the on.		13	60 1288	120 1348	180 1407	
31-MAR-199	id liver spleen INFLS fitied polylinker host=DH: Rsiteal=Pac I Rsite2=Eco conception male fetus oligo(dT) primer [5' TTTTTT 3'], double-strai (Pharmacia), digested will sites of the modified and of normalization. Lili	thostomata; Mar o.	Elliston, K., Hawkins, M., Le, M., Lennon, G., Marra, M., , Soares, M., Tan, F., mson, A., Wohldmann, P. and		tact	others	Length 334; Indels 1; Gaps			acceatgicc 1	
EST clone 123987 5'.	human clone=123987 library=Soares fetal liver spleen INFLS vector=p7730 (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Reitel=Pac I Reitel=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer [5' AACTGGAAGAATTAATTAAATTATTTTTTTTTTTTTTTT	Chordata; Vertebrata; Gnathostomata; Mammalia; atarhini; Hominidae; Homo.	1 (bases 1 to 334) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. an Wilson, R.		Medicine D1, St. Lou free throug	# #884 t		ggaaactctgatgtcctgggatcatgtatgcattgctctagcatctgccaatagttgct 	ttaatccttcctttatgccctcttggggaaagatttaggaagaagaaggeagtcca 	ttcagggaattctggaggcagcttcagtgaggangtcacacgttccacccatgtccc 	ıctgtg 219
	clone=123987 library=Soares fet =pTTT30 (Pharmacia) with a modi illin resistant) primer=M13RP1 and spleen from a 20 week-post clobNA was primed with a Pac I - AAGAATTAAATAAAGATCTTTTTTTTTTTTTTTTTTTTT	a; Chordata; V	N., Dubuque,T., M., Kucaba,T., L., Rohlfing, rston,R., Will	l Project	ject ity School of arkway, Box 85 austl.edu nce stops: 255 ortium, LINI lable royalty- info@image.llr	751294 Location/Qualifiers 1334 /organism="Homo sapiens /otlone="123987" /note="human"	Score Pred.	gatcatgtatgcat 	ctcttggggaaage 	gccttcagtgagga 	aagaaatagtacaa
R01558 334 bp mRNA ye79h02.rl Homo saplens cDNA R01558 EST.	rep1739 (Phaicallin resist. cillin resist. cillin resist. cillin resist. cillin resist. collin was pr. candantAntTAN was ligated to cloned into it. cloned was pr. rinfed hy Pani	Homo sapiens Eucaryotae; Metazoa; Eutheria; Primates;	er, L., Clark, l er, L., Clark, l m, M., Hultman, ns, J., Rifkin, iskis, E., Waten	The WashU-Merck EST Project Unpublished (1995)	Contact: Wilson RK Washid-Merck EST Project Washington University School of it 4444 Forest Park Parkway, Box 85/ Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 259 Source: IMAGE Consortium, LINIL This clone is available royalty— This clone is available royalty— IMAGE Consortium (info@image.lln)	gi: 95 a	14.7 99.5 vativ	tctgatgtcctgg 	cttcctttatgcc }	pattetggaggea 	181 tcaaacaatgtcatttcagaaagaaatagtacaactgtg 219
z	human vector (ampic Liver stranc AACTG CDNA v			ΑΓ	Conta Washu Washi 4444 761: Fax: Emall High Sourc This	NCB1	IGIN Query Match Best Local Similarity Matches 218; Conser	1 ggaaaac 1229 GGAAAAC	61 ttaatcc 1289 TTAATCC	121 ttcaggg 349 TTCAGG	81 tcaaaca
LOCUS DEFINITION ACCESSION KEYWORDS	SOURCE	ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT		FEATURES SOUIC BASE COUNT	ORIGIN Query M Best Lo Matches	0b Qy 12	Db Qy 12	0b 13	Db 13

May 1 16:40 US-08-462-355-1 rst

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human clone=G4756 library=Fetal heart vector=Lambda gt22 host=E. coli Y1090 primer=GGTGCGACCACTCCTGGAGCC Rsitel=NotI Rsite2=SalI mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo df adaptor-primer. SalI adaptors were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yf09b01.rl Homo sapiens cDNA clone 126313 5' similar to qb:W60626
FWET-LEU-PHE RECEPTOR (HUMAN);
                                                                                                                                                                                                                                                                                                                                                     Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 29)
1 Hwang, D.M.; Fung, Y.W.; Hang, R.X., Laurenssen, C.M., Ng, S.H.,
Lam, W.Y., Tsui, K.W.; Fung, K.P.; Waye, M., Lee, C.Y. and Liew, C.C.
Analysis of Expressed Sequence Tags (ESTs) from Fetal and Adult
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                                                                                                 23-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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Pred. No. 3.31e-125;
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                                                                                             R58715 297 bp mRNA EST C4756 Homo sapiens cDNA clone G4756 5' end. R58715
0; Mismatches
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/clone="G4756"
/note="human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: liewcc@utcc.utoronto.ca.
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Best Local Similarity 91.5%;
Matches 108; Conservative
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SOURCE

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Length 466; 3 others 0; Mismatches 36; Indels PROTEIN-COUPLED RECEPTOR RDC1 HOMOLOG (HUMAN); EST Pred. No. 8,03e-18; Score 31; DB 38; 119 t /organism="Homo sapiens" High quality sequence stops: 303 Source: IMAGE Consortium, LLNL **IRNA** Location/Qualifiers 5 Email: est@watson.wustl.edu The WashU-Merck EST Project 109 /clone="29866" /note="human 466 bp Query Match 2.1%; Best Local Similarity 65.0%; 141 c 67; Conservative Unpublished (1995) GDB: G00-402-213 1..466 Homo sapiens ൻ Wilson, R. NCBI gi: Bonaldo. 94 Query Match source DEFINITION ORGANISM TITLE JOURNAL BASE COUNT Matches REFERENCE ACCESSION AUTHORS KEYWORDS SOURCE FEATURES ORIGIN RESULT Locus 염 δ g ð strand cDNA was primed with a Pac I - oligo (dT) primer [57 AACTGGAAGATTAAGATCTTTTTTTTTTTTTTTTTT], double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTTTS vector. Library went through one round of normalization. Library Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; ÷ vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B Liver and spleen from a 20 week-post conception male fetus. 1st This clone is available royalty-free through LLNL; contact the (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI IMAGE Consortium (info@image.llnl.gov) for further information. 65 agttacctgaacctggccgtggctgacttctgtttcacctccactttgccattctcatg 124 118 GGCAATGGGCTGGTGGGTGGCTGGCCTGAAGATGCAGCGGACAGTGAACACAATT 177 125 gtcaggaaggccatgggaggacattggcctttcggctggttcctgtgcaaattcgtcttt 184 238 GCTCACTTGGCTCTCCAGGCACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCC 297 1 (bases 1 to 349)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Gaps human clone=126313 library=Soares fetal liver spleen 1NFLS accatagtggacatcaacttgttcggaagtgtcttcctgatcgccctcatttgc 238 298 TCCATCATTGTCCTCAACATGTTTGGCAGTGTCTTCCTGCTTACTGCCATTAGC 351 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 ö = -= Score 68; DB 35; Length 349; Pred. No. 9.09e-92; Indels constructed by Bento Soares and M.Fatima Bonaldo. Eutheria; Primates; Catarrhini; Hominidae; Homo. 0; Mismatches 83; Washington University School of Medicine 96 t /organism="Homo sapiens" /clone="126313" High qality sequence stops: 315 Source: IMAGE Consortium, LLNL Location/Qualifiers 99 g Email: est@watson.wustl.edu The WashU-Merck EST Project WashU-Merck EST Project /note="human Query Match 4.7%; Best Local Similarity 64.5%; 93 c 151; Conservative Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 1..349NCBI gi: 757096 Homo sapiens Wilson, R. 19 source ORGANISM BASE COUNT Matches 185 REFERENCE AUTHORS JOURNAL FEATURES

ORIGIN

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COMMENT

US-08-462-355-1.rst May 1 16:40

human clone-29866 library-Soares infant brain lNIB vector=Lafmid BA host-DH10B (ampicillin resistant) primer-M13RP1 Rsitel=Not I Rsite2-Hind III Whole brain from a 73 days post natal female. 1st Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)

1 (Lases 1 to 466)

1 (Lases 1 to 466)

1 (Lases 1 to 466)

2 (Lases 1 to 466)

3 (Lases 1 to 466)

4 (Lases 1 to 466)

4 (Lases 1 to 466)

5 (Lases 1 to 466)

6 (Lases 1 to 466)

7 (Lases 1 to 466)

8 (Lases yf89d03.rl Homo sapiens cDNA clone 29866 5' similar to gb:M64749 G ö normalization. Library constructed by Bento Soares and M.Fatima This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 144 cagtggcccatggggaagctcacgtgcaaagtcacacacctcatcttctccatcaacctc 203 259 CAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCCATCATTGTCCTCAACATG 318 13-APR-1995 Gaps Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 the Lafmid BA vector. Library went through one round of .; 0

183 bp

R81583 EST.

ACCESSION

KEYWORDS

SOURCE

DEFINITION

ORGANISM

REFERENCE AUTHORS

12-JUN-1995

TITLE JOURNAL

COMMENT

LOCUS M78084 238 bp mRNA EST 26-MAY-1992 DEFINITION EST01672 Homo sapiens cDNA clone HHCPD60 similar to N-formylpeptide

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RESULT

Query Match

Matches

q ð

BASE COUNT

ORIGIN

source

FEATURES

US-08-462-355-1,rst May 1 16:40

human clone=117822 library=Stratagene lung (#937210) vector=pBluescript SK- host=SOLR cells (kanamycin resistant) primer=-21m13 Rsitel=EcoRI Rsite2=XhoI Normal lung tissue from a 72 human clone=HHCPD60 library=Subtracted Hippocampus, Stratagene (cat. #936205) vector=lambdaZAP-II primer=M13 Forward The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; W138 lung fibroblast cell line; oligo-ff + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988). year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: yel5e04.sl Homo sapiens cDNA clone 117822 3' similar to gb:M60626 ö Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; 1 (bases 1 to 238)
Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C.
Sequence identification of 2,375 human brain genes
Nature 355 (6361), 632-634 (1992) 151 acctttgtcctcggggtcctgggcaacgggcttgtgatctgggtggctggattccggatg 21097 ACTITITACTGGGATTGCCAGGGAATGGGCTGGTGGTGGTGGGGGGCGCCTGGCCTGAGATG 156 Sarcopterygii, Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Gaps 20-MAR-1995 ö Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 238 1 others Score 28; DB 32; Length 238 Pred. No. 6.32e-13; 0; Mismatches 26; Indels The Institute for Genomic Research 932 Clopper Road, Gaithersburg, MD 20878 56 t /organism≃"Homo sapiens" FMET-LEU-PHE RECEPTOR (HUMAN);. mRNA Location/Qualifiers 5 28 /clone="HHCPD60" /gene="D0S1083E" Email: arkerlav@tigr.org. 157 CAGCGGACAGTGAACACAAT 176 211 acacacacaqtcaccaccat 230 /note="human" Contact: Kerlavage AR 497 bp 1.9%; Best Local Similarity 67.5%; Matches 54; Conservative 70 c <1..>238 1..238Tel: 3018699056 Fax: 3018699423 NCBI gi: 273821 Homo sapiens ø 92168112 23 T90501 T90501 EST. EST. Query Match

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COMMENT
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PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);
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                                                                                               i (bases I to 497)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Lafmid BA vector. Library went through one round of
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5'-GAATTCGCCACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTT-3'.
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/clone="117822"
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                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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JOURNAL
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US-08-462-355-1 rst May 1 16:40

Human clone=D2-12 library=Chromosome 19p12-p13.1 exon vector=pAMP10 cosmids from Lawrence Livermore National Laboratory using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88: 4005-4009, 1991). Amplified exons were cloned Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. ö Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. host=E. coli DH5a primer_SD2 : 5' ATC TCA GTG GTA TTT GTC AGC 3 Exons were isolated from human chromosome 19p12-p13.1 specific 104 ggaaactggtactttnggaacttcctatgcaaggcagtccatgtcatctacacagtcaac 163 256 GGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCCATCATTGTCCTCAAC 315 Gaps 03-JUL-1995 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 0; 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Length 249; 5 others 0; Mismatches 42; Indels 164 ctctacagcagtgtcctcatcctggccttcatcagtctggaccgnt 209 into pAMP10 by uracial cloning (GIBCOL BRL). H14008 198 bp DNA EST EST00034 Homo sapiens genomic clone D2-12 5' H14008 Washington University School of Medicine Score 24; DB 12; Pred. No. 6.35e-07; 56 t /organism="Homo sapiens" High quality sequence stops: 198 Source: IMAGE Consortium, LLNL Location/Qualifiers σ Email: est@watson.wustl.edu The WashU-Merck EST Project 55 /clone="49725" Contact: Wilson RK WashU-Merck EST Project /note="human" 1.7%; 75 c 1 (bases 1 to 249) 64; Conservative Unpublished (1995) Fax: 314 286 1810 Tel: 314 286 1800 1..249 GDB: G00-422-535 NCBI gi: 900013 Homo sapiens Best Local Similarity Wilson, R. 28 EST. Query Match source RESULT 14 DEFINITION ORGANISM BASE COUNT TITLE Matches REFERENCE AUTHORS ACCESSION FEATURES KEYWORDS

May 1 16:40

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Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 198)

REFERENCE

Li,Q.Y. Unpublished (1995)

AUTHORS JOURNAL COMMENT

Map: Chromosome19p12-p13.1

Human Molecular Genetics

Contact: Li QY

Queen's Medical Centre Nottingham, NG7 2UH, UK

Tel: 1159249924 Fax: 1159709906

NCBI gi: 888021 source FEATURES

1..205

/clone="D2-32

/note="Human" <1..>205

36 t 42

BASE COUNT

33 tgcaccttctcggcacccagccacagcaccagcctcctgcagggc 77

158 TGCATCTTCAGGCCAGCCACCCACGCACGGCCCATTGCCTGGC 114

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Email: pdzqyl@pdn1.gene.nottingham.ac.uk.

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Query Match 1.6%; Score 23; DB 7; Length 198; Best Local Similarity 75.6%; Pred. No. 1.55e-05;

Query Match

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/map="19p12-p13.1" 72 c 49 q

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mRNA

/organism="Homo sapiens" /clone="D2-12" /note="Human"

Location/Qualifiers

NCBI gi: 888017

1..198

source

FEATURES

03-JUL-1995

H14012 205 bp DNA EST EST00038 Homo sapiens genomic clone D2-32 5'.

H14012

ACCESSION KEYWORDS

SOURCE

LOCUS RESULT 15

Human clone=D2-32 library=Chromosome 19p12-p13.1 exon vector=pAMP10 host=E. coli DH5a primer=SD2 : 5' ATC TCA GTG GTA TTT GTC AGC 3' Exons were isolated from human chromosome 19p12-p13.1 specific cosmids from Lawrence Libremore National Laboratory using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88: 4005-4009, 1991). Amplified exons were cloned into pAMP10 by uracial cloning (GIBCOL BRL).

Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria,

Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

ORGANISM

Eutheria, Archonta, Primates; Catarrhini, Hominidae, Homo-1 (bases 1 to 205)

Map: Chromosome19p12-p13.1 Contact: Li OY Human Molecular Genetics

Unpublished (1995)

AUTHORS JOURNAL COMMENT

REFERENCE

Queen's Medical Centre Nottingham, NG7 2UH, UK

Tel: 1159249924 Fax: 1159709906

Email: pdzqyl@pdn1.gene.nottingham.ac.uk.

US-08-462-355-1.rst

Location/Qualifiers

/organism="Homo sapiens"

/map="19p12-p13.1" 73 c 54 q

Query Match 1.6%; Score 23; DB 7; Length 205; Best Local Similarity 75.6%; Pred. No. 1.55e-05; Matches 34; Conservative 0; Mismatches 11: Thatle ORIGIN

Search completed: Wed May 1 16:48:31 1996 Job time : 607 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn MasPar time 896.41 Seconds 1142.027 Million cell updates/sec Wed May 1 16:20:37 1996; Run on:

Tabular output not generated.

>US-08-462-355-1 (1-1446) from US08462355.seq 1446 Description: Title:

1 ATGCGTCTTTCTCTGCTGA......AAAGAAATAGTACAACTGTG 1446
TACCGCAGAAAGAGACGACT......TTTCTTTATCATGTTGACAC Perfect Score: N.A. Sequence:

Gap 6

TABLE default

Scoring table:

264399 seqs, 353985056 bases x 2 Searched:

Dbase 0; Query 0

STD:

Nmatch

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

embl-new11

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PR11 10:PR12 11:PR13 12:PR01 13:PR02 14:R0D 15:SYN 16:UNC 17:VRT 18:VIR

Database:

genbank91
19;BCT1 20;BCT2 21;BCT3 22;BCT4 23;BCT5 24;BCT6 25;BCT7
26;INV1 27;INV2 28;INV3 29;INV4 30;INV5 31;MAM1 32;MAM2
33;PAT1 34;PAT2 35;PAT3 36;PHG 31;PIM1 38;PLM2 39;PLM3
40;PLM4 41;PLM5 42;PLM6 43;PLM7 44;PRI1 45;PRI2 46;PRI3
47;PRI4 48;PRI5 49;PRI6 50;PRI7 51;PRI8 52;PRI9 53;ROD1
54;ROD2 55;ROD3 56;ROD4 57;ROD5 58;ROD6 69;RD1
61;SYN 62;UNA 63;VRL1 64;VRL2 65;VRL3 66;VRL4 67;VRL5
66;VRL6 69;VRT1 70;VRT2 71;VRT3

Database:

genbank-newll 72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA 86:VRL 87:VRT

u-emb144_91

Database:

88:part1

Mean 11.585; Variance 3.952; scale 2.932

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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	OI OI		HSCSANAPL	HSC5AR	HUMC5AAR	HUMNFPR	HUMFMLP 26	HUMFMLP	HUMFPR1A	RABFPR	CFCOMC5AM	HIIMEMI,PX	HIIMPEPROA	HSFPRHO	нимимез	HUMFPR1.1A	HIJMFRP1.2	\$5057782	MUSCSAGPR	HIJMFMI,PY	MUSNEORREC	574702	HSU13666	HUMCR	HSU03642	CFGPCR1	HS334481	HSU33448	RRVTIAIIR	RATATIB	S77863	S37491	HSU17298	HS224911	HSU22491	HUMOPRK1B	MMMOR3	RNU02083	HSU12569	RATMORA	MMU26915	MM26915	HSU07225	HS07225	RATMUOR1A	HUMMOR1X	RATRORB
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ALI GNMENTS

02-JUN-1992 HSC5ANAPL 1080 bp DNA PRI H.sapiens RNA for receptor for C5a anaphylatoxin. X58674 DEFINITION ACCESSION KEYWORDS RESULT Locus

C5a anaphylatoxin receptor. human. ORGANISM SOURCE

Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

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REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuteroscomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; ö 166 gccctggtggtctgggtgacggcattcgaggccaagcggaccatcaatgccatctggttc 225 244 TTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCCATC 303 346 atcctgctcaacatgtacgccagcatcctgctcctggccaccatcagcgccgaccgcttt 405 304 ATTGTCCTCAACATGTTTGGCAGTGTCTTCCTGCTTACTGCCATTAGCCTGGATCGCTGT 363 ctgctggtgtttaaacccatctggtgccagaacttccgaggggccggcttggcctggatc 465 525 424 ATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGTTGTGCATTCCTGTGTTCGTGTACCGG 483 Gaps 13-NOV-1992 ö Gerard, N.P. and Gerard, C.
The chemotactic receptor for human C5a anaphylatoxin
91156029 Score 91; DB 44; Length 1080; Pred. No. 1.02e-67; 0; Mismatches 165; Indels HSC5AR 1092 bp RNA PRI H.sapiens C5aR rRNA for C5 anaphylatoxin receptor. X57250 /organism="Homo sapiens" Catarrhin; Hominidae; Homo. 1 (bases 1 to 1080) Location/Qualifiers 292 g C5a anaphylatoxin receptor. Best Local Similarity 60.8%;
Matches 256. 343 c 256; Conservative 1..1080 NCBI gi: 29568 Homo sapiens æ 189 human. 526 g 526 484 G 484 DEFINITION ACCESSION KEYWORDS 7 SOURCE ORGANISM source BASE COUNT 406 JOURNAL MEDLINE REFERENCE FEATURES COMMENT ORIGIN LOCUS

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MGLALLLLTIPSFLYRVVREEYFPPKVLCGVDYSHDKRRRRAVAIVRLVLGFUMPLLTL
TICYTFILLRTWSRRATRSTKTLKVVAVVAVVASFFIFMLPYQVTGIMMSFLEPSSPTFL
LLNKLDSLCVSFAYINCCINPIIYVAGQGFQGRLRKSLPSLLRNVLTEESVVRESKS
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AVVFLVGVLGNALVVWVTAFEAKRTINAIWFLANLAVADFLSCLALPILFTSIVQHHHW
                                                                                                                                                                                              Human peripheral blood promyelocytic leukemia cell line HL-60 (ATCC CCL 240), cDNA to mRNA, clone C5a-receptor.
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                                                                                                                    06-MAR-1995
                                                                                                                                                                                                                                                            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                      Boulay, F., Mery, L., Tardif, M., Brouchon, L. and Vignais, P. Expression cloning of a receptor for C5a anaphylatoxin on
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/note="potential translated region; putative;
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                                                                                                                                     Human C5a anaphylatoxin receptor mRNA, complete cds.
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/product="C5a_anaphylatoxin_receptor"
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/sequenced_mol="cDNA to mRNA"
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/clone="C5a-Receptor"
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Matches 256; Conservative
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TIVDINLEGSVELIALIALDRCVCVLHPVWTQNHRTVSLAKKVIIGPWVMALLLTLPV IIRVTTVPGKTGTVACTFNFSPWTNDPKERINVAVAMLTVRGIIRFIIGFSAPMSIVA Boulay, F., Tardif, M., Brouchon, L. and Vignais, P. Synthesis and use of a novel N-formyl peptide derivative to isolate /translation="METNSSIPTNISGGTPAVSACYLFLDIITYLVFAVTFVLGVLGN GLVIWVAGFRMTHTVTTISYLALAVADFCFTSTLPFFWVRKAMGGHWPFGWFLCKFLF VSYGLIATK HKQCLIKSSPPLRVLSFVAAAFFLCASPYQVALIATVRIRELLQCMY KEIGIAVDVTSALAFFNSCLMPMLYVFMGQDFRERLIHALPASLERALTEDSTQTSDT ö 370 atcctgctcaacatgtacgccagcatcctgctcctggccaccatcagcgccgaccgctt 429 244 TIGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCCATC 303 02-APR-1991 5' end. Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; **;** Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. /product="N-formylpeptide receptor fMLP-R98" Score 89; DB 51; Length 1050; Pred. No. 1.73e-65; Biochem. Biophys. Res. Commun. 168, 1103-1109 (1990) 0; Mismatches 116; Indels HUMNFPR 1050 bp mRNA PRI Human N-formylpeptide receptor fMLP-R98 ORF mRNA, /sequenced_mol="cDNA to mRNA" 1..1050 a human N-formyl peptide receptor cDNA 280 t /organism="Homo sapiens" /note="NCBI gi: 189184" Location/Qualifiers б ATNSTLPSAEVALQAK" N-formyl peptide receptor. /codon start=1 Query Match 6.2%; Best Local Similarity 63.9%; Matches 205; Conservative (bases 1 to 1050) /label=0RF Human cDNA to mRNA. 300 1..1050 /partial NCBI gi: 189183 Homo sapiens 90267449 215 g 550 G 484 source BASE COUNT ORIGIN SOURCE ORGANISM DEFINITION 364 490 550 484 MEDLINE REFERENCE AUTHORS JOURNAL ACCESSION CDS KEYWORDS FEATURES TITLE COMMENT RESULT Locus

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167 accttgtcctcggggtcctgggcaacgggcttgtgatctgggtggctggattccggatg 			Db 407 ategecetcattgetetggacegetgtgtttgegteetgeatecagtetggaceagaae 466	467 caccgcaccgtgagcctggcc 487 	RESULT 6 LOCUS HUMFMLP 1866 bp mRNA PRI 23-JAN-1991 DEFINITION Human N-formylpeptide receptor (fMLP-R98) mRNA, complete cds. ACCESSION M60626 M33537 KEYMORDS N-formyl peptide receptor; N-formylpeptide receptor fMLP-R98. SOURCE Human, cDNA to mRNA.	ORGANISM Homo sapiens Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eukaryota; Animates; Haplorhini; Catarrhini; Hominidae. Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. 1 (bases 1 to 1866) AUTHORS Boulay, F., Tardif, M., Brouchon, L. and Vignais, P. TITLE The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-Protein-Coupled	receptors JOURNAL Biochemistry 29, 11123-11133 (1990) MEDLINE 91105045 COMMENT NCBI gi: 182662 FEATURES Location/Qualifiers	source 11866 /organism="Homo sapiens" /sequenced_mol="cDNA to mRNA" mRNA <11866 CDS 461098		ATNSTLPSAEVALQAR" BASE COUNT 457 a 471 c 469 g 469 t ORIGIN	Query Match 6.2%; Score 89; DB 49; Length 1866; Best Local Similarity 63.9%; Pred. No. 1.73e-65;
Db 106 acctttgtcctcggggtccttgggcaacgggcttgtgatctgggtggctggattccggatg 165	<pre>dy 157 cacccacactcaacactartcatrccrccaccrcaccaccrccrccrccrccrccrccrccrc</pre>	286 ttcctgtgcaaattcctctttaccatagtggacatcaacttgttcggaagtgtcttcctg	Db 346 atcgccctcattgctctggaccgctgtgtttgcgtcctgcatccagtctggacccagaac 405 	Db 406 caccgcaccgtgacctggcc 426 	RESULT 5 LOCUS HUMFMLP26 1281 bp mRNA PRI 23-JAN-1991 DEFINITION Human N-formylpeptide receptor (fMLP-R26) mRNA, complete cds. ACCESSION M60627 M33538 KEYWORDS N-formyl peptide receptor; N-formylpeptide receptor fMLP-R26. SOURCE Human, cDNA to mRNA. ORGANISM Homo sapiens	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. REFERENCE 1 (bases 1 to 1281) AUTHORS Boulay, F., Tardif, M., Brouchon, L. and Vignais, P. TITLE The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-Protein-Coupled receptors	JOURNAL Biochemistry 29, 11123-11133 (1990) MEDLINE 91105045 COMMENT NCBI gi: 182664 FEATURES Location/Qualifiers source 11281	/organism="Homo sapiens" /sequenced_mol="cDNA to mRNA" <11281 CDS 62114 /note="MCNI oi: 182665"	/nocen retail ji. 10200 /rodon_start=I /product="N-formylpeptide_receptor_fMLP-R26" /translation="WaffaySilPTWISGCTPAYSACTIFIDITYIVFAYTFVLGVLGN GLVIWVAGFRHTHVTTSYIMLAVADFCFTSTLPFFFWRKAMGGHWPFGWFLCKFVF TIVOTNLEGSFRIALIARCVCVIAFWTQNHRTVSIAKGVIIGPWWALLLILILVV IIRVTTVPGKTGTVACTFNFSPWTNDPKERINVAVAMLTVRGIIRFIIGFSAPMSIVA VSGLIATKTIKRQGLIKSSRPIRVISFVAAAFFLOMSPYQVALIATVRIRELIGGMY KEIGIAVDVTSALAFFNSCIAPMLYVFWGQDFRERLIHALPASIERALTEDSTGTSDT ATNSTLPSAEVELOAR"	285 a 353 c 313 g 330 t	Query Match 6.2%; Score 89; DB 49; Length 1281; Best Local Similarity 63.9%; Pred. No. 1.73e-65; Matches 205; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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                                    acctttgtcctcggggtcctgggcaacgggcttgtgatctgggtggctggattccggatg 210
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; G protein coupled receptor; N-formyl peptide;
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Homo sapiens (library: Lambda FIX) DNA.
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US-08-462-355-1.rge 479..552 /gene="FPR1" /number=1 May 1 16:28 exon

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Gaps ; 0 Length 6931; 0; Mismatches 116; Indels Score 89; DB 49; Pred. No. 1.73e-65; Best Local Similarity 63.9%; Matches one. 205; Conservative Matches

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5486 acctttgtcctcggggtcctgggcaacgggcttgtgatctgggtggctggattccggatg 5545

5546 acacacagteaceaceateagttacetgaacetggeegtggetgaettetgttteace 5605

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AMAVALLLTVPSF IFRCYHTEYFPFMMTCCVDYSCYCVLVERCVAILRLLMCFLGPLV ILSICYTFLLIRTMSRKATRSTKTLKVVVAVVVSFFVLMLPYQVTCMMMALFYKHSES FRRVSRLDSLCVAVAYINCCINPIIYVLAAQGFHSRFIKSLPARLRQVLAEESVGRDS KSITLSTVDTPAQKSQGV" ö receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19 catectgeteaacatgtaegecageatettgeteetgaecaecateagegeegaeegett 422 483 ggcctgcagcgtggcctgggccgtggccctgctgctgaccgtaccctcgttcatcttccg 542 Bao, L., Gerard, N.P., Eddy, R.L. Jr., Shows, T.B. and Gerard, C. Mapping of genes for the human C5a receptor (C5AR), human FMLP cttcctggtggtctgggtgacgggtttcgaggtccggcgaaccatcaatgccatctggtt 242 123 TGGGCTGGTGCTGGTGGCTGGCTGGCCTGAAGATGCAGCGGGACAGTGAACACAATTTGGTT 182 243 teteaacetggeggtggeegateteetgteetgeetggegetgeeeateetgtttegte 302 categiccagcagggetactggccetttggcaacgetgcctgccgcatectgcctcgct 362 CATTGTCCTCAACATGTTTGGCAGTGTCTTCCTGCTTACTGCCATTAGCCTGGATCGCTG 362 tgtcttggtgtttaatcccatctggtgccagaactaccgagggccccagctggcctgggc 482 363 TCTTGTGGTATTCAAGCCAATCTGGTGTCAGAATCATCGCAATGTAGGGATGCCCTGCTC 422 Homo sapiens (tissue library: human genomic) lung cDNA to mRNA CCCAGTAATTCTCTCCATGGTCATTCTCAGCCTTACTTTTTACTGGGATTGCCAGGCAA 122 complete cds Gaps Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; ö Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. 1 (bases 1 to 1058) Score 86; DB 31; Length 1993; Pred. No. 3.71e-62; 0; Mismatches 167; Indels HUMFMLPX 1058 bp mRNA PRI Human FMLP-related receptor II (FMLP R II) mRNA, FMLP-related receptor II; GTP-binding protein; plasma membrane protein; protein coupled /organism="Homo sapiens"
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SOURCE

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FLETTYTIENGDTYCFFURASWGGTPEERLKVA I WITTARCII IRVI GFSLEMSIVA
I CYGLIAAKIHKKCMIKSSRPLRVITAVVASFFI CWFPFQLVALLGTVWLKEMLFYGK
YKI IDII UND TSSLAFFNSCLAPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTND
TAANSASPPAETELQAM"
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Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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Pred. No. 6.03e-60;
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532 gtcctgcatccagtctgggcccagaaccaccgcactgtgagtctggcc 579 370 g ð

13 RESULT

Catarrhini; Hominidae; Homo.

LOCUS DEFINITION	HUMHM63 1910 bp mRNA PRI 17-FEB-1994 Human mRNA for FMLP-related receptor (HM63).	250
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REFERENCE AUTHORS TITLE	H	SULT 14
JOURNAL MEDLINE COMMENT	Int. Immunol. 5, 1239-1249 (1993) 94092629 Submitted (13-Apr-1992) to DDBJ by: Hideki Nomura	myl peptidė red
	•	Σ
	Phone: 0762-62-8151 x5875 Fax: 0762-60-7704.	REFERENCE 1 (bases 1 to 2631) AUTHORS Murphy, B.M., Ozcelik, T., Kenney, R.T., Tiffany, H.L., McDermott, D.
FEATURES	NCBI gi: 219864 Location/Qualifiers	TITLE A structural homologue of the N-formyl peptide receptor. Characterization and chromosome mapping of a peptide
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	FILFLTTYTIPNGDTYCTFNFASGGTPEERIKVAITMITARGIIRFYIGFSILPMSIVA ICYQLIARAHHKKOMIKSSRPLAKYLTAVASFFICMFRPQILALLGTVMIKEMLIFGK VXTITITIANDFGGIAFENGYAYAVYONDEDDIIHGIDFGIAFGEDAN	/map=19" /note="Note" i: 182742" /note = note = not
BASE COUNT	TANISASPPETEIGAM" 18 4 406 c 415 g 621 t	/qbxxef="G00-127-554" /product="formyl peptide receptor"
ORIGIN		/translation="METNESTPINEYEEVSYESAGYTVLATIEPLVULGVTEVLGN GLVIWVAGERMFRTVTTICTULALAESSTFATLETLVSHAMGEKWEFGRELOK
Query Match Best Local	5.8%; Score 84; DB 50; Length 1910; Similarity 62.1%; Pred. No. 6.03e-60;	IVVDINIEGSVE LIGE FALDRCITO LERVARQURRIVS LAMRO I VERWILARU KI FLELTTVI TINODIV CTRIPA SNGGOPERELKKAN THLITARGIT I FRUI GESLENS TANGTITA SAKTI UKRCATIV GEODI DIVI MANINA GEPET GEDEGATIVA I TOWINA KEWIE
Jato	(10) CONSELVATIVE U; MARMACCHES 132; INDELS U; GADS U;	LUIGLIAMAI HANNAILESSAK LANVIALEN KORTEKULERIKULASIA VIITAKAPLAS YKI IDILUMYISSLAEFINSCLAPMLYVFVGQDFRERLIHSLEPTSLERALISEDSAP maaanse odda tempi sempi odali
07 70	<pre>113 accecccatcggtggtggtgaccttgtcctcgggccetgggcatcgggcatcgggcct 1/2 11 </pre>	polyA_site 2631 /gene="FPRL1" /~~~~10"
0b 173 Qy 130	173 gtgatctgggtggctggattccggatgacacgcaccatctgttacctgaac 232 	/map/_
Db 233 Qy 190	233 ctggcctggctgactttctttcacggccacattaccattcctcattgtctccatggcc 292 	Query Match 5.8%; Score 84; DB 49; Length 2631; Best Local Similarity 62.1%; Pred. No. 6.03e-60; Matches 216; Conservative 0; Mismatches 132; Indels 0; Gaps

293 atgggagaaaaatggccttttggctggttcctgtgtaagttaattcacatcgtggtggac 352

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FIALDRCICVLAPVWAQNHRTVSLAMKVIVGPWILALVLTLEV CCTENEASWGCTPEERLKVAITWLTARGIIRFVIGESLEPMSIVA HIKSSRPIRVLTAVVASFFICMFPFQLVALLGTVWIKEMLFYGK FFNSCINPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTND PAM" ETNF STPLMEYEEVS YESAGYTVLR I LPLVVLGVTFVLGVLGN TTI CYLMLALADF SFTAT LPFLI VSMAMGEKMPFGWFLCKLI H mRNA PRI 08-NOV-1994 eptor-like receptor (FPRLI) mRNA, complete ö Kenney, R.T., Tiffany, H.L., McDermott, D. 851 atcctcccattggtggtgtgtggggtcacctttgtcctcggggtcctggggcaatgggtt 910 Mismatches 132; Indels 0; Gaps or; peptide chemoattractant receptor. to mRNA. rdata; Vertebrata; Mammalia; Theria; omosome mapping of a peptide receptor. comosome mapping of a peptide family 7637-7643 (1992) orhini; Catarrhini; Hominidae. ore 84; DB 49; Length 2631; ed. No. 6.03e-60; l peptide receptor" .lt" ="cDNA to mRNA" 793 uo sapiens" 50" trpohil" 182742" .554 * iers Вþ

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/product="N-formyl peptide receptor-like 2 protein" /translation="METNFSIPINETEEVIDEPACHTVIMIFSLIVHGVTFVFGVIGN GLVIWVAGFRWTRTVVNTICYINIALADFSFSAILPFRMVSVAMREKWPFGSFLCKLVH VMIDINLFVSVYLITIIALDRCICVLHPAMAQNHRTMSLAKRVWTGLMIFTIVLTLPN Human N-formyl receptor-like 2 protein (FPRL2) gene, complete cds. ö 1 (bases 1 to 1198) Durstin, M., Gao, J.L., McDermott, D. and Murphy, P.M. Structural and functional analysis of the human N-formyl peptide N-formyl peptide receptor-like 2 protein; transmembrane protein. Homo sapiens (tissue library: lambda FIX; Stratagene) adult DNA. Homo sapiens 971 ctggccctggctgacttttctttcacggccacattaccattcctcattgtctccatggcc 1030 130 GTGCTGTGGGTGGCTGGCCTGAAGATGCAGCGGACAGTGAACACAATTTGGTTCCTCCAC 189 70 ATTCTCTCCATGGTCATTCTCAGCCTTACTTTTTACTGGGATTGCCAGGCAATGGGCTG 129 Gaps 08-NOV-1994 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; 911 gtgatctgggttggttggattccggatgacacgcacagtcacccatctgttacctgaac ö Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Score 76; DB 49; Length 1198; Pred. No. 3.47e-51; 0; Mismatches 127; Indels /tissue lib="lambda FIX; Stratagene" 80..1141 /organism="Homo sapiens" /dev_stage="adult" /sequenced_mol="DNA" /note="NCBI gi: 292035" /gdb_xref="G00-128-855" 264 g Location/Qualifiers DNA /map="Unassigned" /codon start=1 /gene="FPRL2" receptor gene cluster 1198 bp Best Local Similarity 61.5%; Matches 203; Conservative 301 c Unpublished (1993) NCBI gi: 292034 HUMFRP L.2 280 L14061 Query Match 15 source DEFINITION ORGANISM BASE COUNT 1091 ACCESSION KEYWORDS SOURCE AUTHORS JOURNAL REFERENCE S FEATURES TITLE COMMENT

US-08-462-355-1.rge May 1 16:28

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222 tctgggtggctggattccggatgacacgcacagtcaacactttgttacctgaacctgg 281 282 occtagotgacttctctttcagtgccatcctaccattccgaatggtctcagtcgccatga 341 ccrrecessactectestestestestes 253 162 teteattgetagtecaeggagteaeetttgtetteggggteetgggeaatgggettgtga 194 a 쇰 g q ð ð ð Ş ð

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Wed May 1 16:36:07 1996, MasPar time 111.87 Seconds 859.505 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-462-355-1 (1-1446) from US08462355.seq 1446

Description: Perfect Score: N.A. Sequence:

1 ATGCCGTCTTTCTCTCTGTGA......AAAGAAATAGTACAACTGTG 1446
TACCGCAGAAAGAGACGACT......TTTCTTTATCATGTTGACAC

Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 84802 segs, 33246950 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq22 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Mean 9.408; Variance 5.327; scale 1.766 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB 1D c 1 85 5.9 1047 2 010572 c 3 47 3.3 204 1 N81164 c 4 43 3.0 91 9 051746 f 41 2.8 204 1 N81164 f 40 2.8 1872 11 066176 f 40 2.8 1872 11 066176 f 41 2.8 204 1 081164 f 40 2.8 1872 11 066176 f 41 2.8 209 11 066176 f 43 2.4 114 12 070469			~					
85 5.9 1047 2 6 6 4.3 1047 2 6 4 3 3.3 204 1 6 4 1 2.8 204 1 1 4 0 2 8 1 1 1 3 8 2.4 1 1 4 1 2 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 1 4 12 6 2098 1 1 6 3 8 2.4 1 4 12 6 2098 1 1 6 3 8 2.4 1 4 12 6 2098 1 1 6 3 8 2.4 1 4 12 6 2098 1 1 6 3 8 2.4 1 4 12 6 2098 1 1 6 3 8 2.4 1 4 12 6 2098 1 1 6 3 8 2 6 2098 1 6 2 6 2098 1 6 2 6 2098 1 6 2 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Resul			Tonath	ä	E	Description	Pred No.
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204 1 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	ູ່	1 85	5.9	1047	7	010572	Human Natriuretic Pep	1.63e-39
204 1 1 91 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		2 62	4.3	1047	7	010572	Human Natriuretic Pep	5.41e - 24
91 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	υ	3 47	3.3	204	~	N81164	Base substituted E.co	2.42e - 14
204 1 1 1872 11 (2098	U	4 43	3.0	91	9	051746	Oligonucleotide probe	•
204 1 1 1872 11 0 2098 11 0 114 12 0		5 42	2.9	91	9	951746	Oligonucleotide probe	
1872 11 (2098 11 (114 12 (/	6 41	2.8	204	-	N81164	Base substituted E.co	1.18e - 10
2098 11 (/	7 40	5.8	1872	Ξ	066176	Seven transmembrane r	4.74e - 10
114 12 (1	8 38	2.6	2098	11	066177	Seven transmembrane r	7.38e-09
		34	2.4	114	12	070469	Generic DNA sequence	1.57e - 06

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Generic DNA sequence	DNA	DNA	Generic DNA sequence	Generic DNA sequence	Seven transmembrane r	Generic DNA sequence	Human kappa opioid re	Epsilon opioid recept	Generic DNA sequence	Generic DNA sequence	Partial sequence of t	Human mu opioid recep	Transcription regulat	Rat mu opioid recepto	Human P20 receptor ge	Partial sequence of t	Rat mu-subtype opioid	Human mu opiate recep	HSV-1 gB and surround	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	Seven transmembrane r	Generic DNA sequence	Sequence encoding new	Sequence encoding new	Sequence encoding new				Sequence encoding new	Rat opioid receptor c	Rat opiorph receptor
Q70465 070470	070467	070468	070469	070465	066173	070467	075931	083681	070466	070468	056703	089226	089223	089222	088134	056705	079199	093102	N71302	070472	070466	Q70470	070471	066150	970472	N50034	N50031	N50032	N50027	N50033	N50028	N50023	089233	092972
12	12	12	13	12	Ξ	12	13	15	12	12	10	15	15	15	15	10	12	15	7	12	12	13	12	1	12	٣	m	٣	ო	m	ო	m	15	16
114	114	114	114	114	720	114	1000	1054	114	114	829	1610	1618	1618	1842	1981	2070	2160	3871	114	114	114	114	120	114	498	501	501	501	501	501	501	1567	2706
2.4	2.4	2.4	2.4	2.4	2.4	2.3	2.3	2.3	2.2	2.2	2.2	2.5	2.5	2.5	2.2	2.5	2.2	2.5	2.5	2.1	2.1	2.1	2.0	2.0	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
34	34	34	34	34	34	33	33	33	35	32	32	32	32	32	35	32	32	32	32	30	31	31	59	53	87	27	27	27	27	27	27	27	88	78
10	12	13	14	15	16	11	18	19	70	21	22	23	24	52	56	27	88	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Modified -site 161..163 Modified -site 195.197 'label= N-qlycos site /label= N-glycos site

'label= N-glycos_site

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88; Conservative 279; Mismatches 597; Indels 12;

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DB 2; Length 1047;

Score 85; DB 2; L Pred. No. 1.63e-39;

5.9%; 9.0%;

Best Local Similarity

Matches

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51 T;

83 G;

15 C;

87 A;

1047 BP;

Sequence Query Match

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114,952).

23-JUN-1989; US-370673. (GETH) GENENTECH INC. Chang M, Goeddel D, Lowe D; WPI; 91-036711/05.

N-PSDB; Q10324.

22-JUN-1990; U03586.

/label= N-glycos site Modified -site 777..279 /label= N-glycos site Modified -site 349..351 Modified -site 244..246

/label= N-glycos site Modified -site 600..602

/label= N-glycos_site

W09100292-A. 10-JAN-1991.

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91 thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnn 150 / Match 3.3%; Score 47; DB 1; Length 204; Local Similarity 11.6%; Pred. No. 2.42e-14; 11; Conservative Escherichia coli. : : 773 TATT 776 misc feature dnnd 901 05-MAY-1988. primer_bind EP-285123-A. Sequence Query Match N81164; /*tag= 868 Matches ð 유 ð 셤 ð a ò 셤 õ a 9 360 dgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnw 419 420 wtgrnnnwykgannsdnnncandnddnscdktnnstnanvangtgntnnmngvssnnnnr 479 480 knmnnknnasmnwrnrwnnnngnsnryhkgagsrntnsnrgssygsnmtahgkynnnan 539 540 tghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndnnnncnvtnyc 599 414 GCCCTGCTCTATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGTTGTGCATTCCTGTGT 473 600 nrgsnndnnndsnnndmnrysnnndnvkgmannhnsnnsshgsnkssncvvdsrnvnk 659 660 ntdyqnasnrstannddnnanyakknntannnnsqnnnnttqmnaadvysnqnnnnnan 719 237 GCTCACTTGCCTCTCCAGGGACAGTGCCCTACGCCAGGTTCCTATGCAAGCTCATCCC 296 Gaps NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr= The sequence was derived from the DNA encoding natriuretic peptide kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English. 9 affinity chromatography. Antibodies with affinity for NPRB DB 2; Length 1047; 55; Conservative 150; Mismatches 333; Indels 51 T; 83 G; Pred. No. 5.41e-24; /note= "GC and protien kinase activity" 4.3%; Score 62; 15 C; 87 A; Chang M, Goeddel D, Lowe D; Best Local Similarity 10.1%; /label= N-glycos site Modified -site 161..163 /label= N-glycos site Modified -site 244..246 /label= N-glycos site Modified -site 277..279 /label= N-glycos site Modified -site 195..197 /label= N-glycos site Modified -site 349..351 /label= N-glycos_site Modified -site 600..602 23-JUN-1989; US-370673. /label= N-glycos site Modified -site 35..37 /label= N-glycos_site (GETH) GENENTECH INC. 22-JUN-1990; U03586. 1047 BP; WPI; 91-036711/05. N-PSDB; Q10324. Modified -site also be prepd 10-JAN-1991. W09100292-A 114,952). Sequence Query Match Matches

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720 rsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnnnmnrcwandnanrndn 779 780 gnnkgnnrrnn-knggtsnndnnnnrmnnyannnnknvnnrtnaynnnkrkanannynnn 838 654 AAATGATCATCCTTGGACAGTCCCCACTGTCTTCCAACCTCAAACATTTC-AAAGACCTT 712 839 nhsvannnkrgntvnanandsvtnyns-dnvgntansanstnmnvvtnnndnytcndann 897 713 CTGCAGATICACTCCCTAGGGGTTCTGCTAGGTTAACAAGTCAAAATCTGTATTCTAATG 772 by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening. Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which transcriptase and the molecules are completed to forms that can be single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all E.coli beta galactosidase alpha-fragment; base substitutions; ss. 47 C; 17 G; 11 T; 108 Others; variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the (SUSO) SUOMEN SOKERI OY. Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; WPI; 88-279927/40. possible nucleotide positions within a specified region. The Base substituted E.coli beta-qalactosidase alpha-fragment. Introducing random point mutations into nucleic acods occurred singularly in any given mutant. See also P80575. Location/Qualifiers /*tag= a /function=multiple cloning site N81164 standard; DNA; 204 BP 204 BP; 21 A; 08-NOV-1990 (first entry) 30-MAR-1988; 105163. 03-APR-1987; US-034819.

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Gaps

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Pred. No. 2.42e-14; 53; Mismatches 31; Indels

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ö Gaps Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may New oligo:nucleotide probes specific for Mycobacteria - used for ö detection and amplification of Mycobacteria nucleic acid in be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. 5; Indels Score 43; DB 9; Length 91; Pred. No. 7.19e-12; 4 T; 15 6; 46; Mismatches 17 C; Claim 3; Page 14; 23pp; English. 3.0%; Best Local Similarity 3.8%; 2; Conservative 91 BP; Sequence Query Match samples Matches

(BECT) BECTON DICKINSON CO.

Spears PA;

Shank DD,

WPI; 93-378844/48.

24-MAY-1993; 108325. 26-MAY-1992; US-889651.

EP-571911-A. 01-DEC-1993

Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; LT 5 Q51746 standard; cDNA; 91 BP. Oligonucleotide probe MK14-A 31-MAY-1994 (first entry) Synthetic. 051746; RESULT

160 GCTGCATCTTCAGGCCAGCCACCCACAGCACCAGCCCATTGCCTGGCAATGCC 108

8 gcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsv 60

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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in Claim 3; Page 14; 23pp; English. (BECT) BECTON DICKINSON CO. Shank DD, Spears PA; EP-571911-A. 01-DEC-1993. 24-MAY-1993; 108325. 26-MAY-1992; US-889651. WPI; 93-378844/48 samples ID AC DIT OF BEACH OF

(Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may

40 CTCTCACAGCCATGGAATGAGCCCCCAGTAATTCTCTCCATGGTCATTCTCAGGCTTACT 99

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Gaps ö be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. 6; Indels Pred. No. 2.93e-11; Score 42; DB 9; 15 6; 43; Mismatches 17 C; Query Match 2.9%; Best Local Similarity 9.3%; 5; Conservative 91 BP; Sequence Matches 888

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1371 CTTCAGTGAGGAGCTCACACGTTCCACCACTGTCCCTCAAACAATGTCATTTC 1424 3 ctccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhv 56 염 ð

77 cdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhy 136 by prepn of single stranded template, annealing a primer, elongation, 60; Mismatches 38; Indels 1; Gaps amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misinorporated by the transcriptase and the molecules are misinorporated by the E.coli beta galactosidase alpha-fragment; base substitutions; ss. 11 T; 108 Others; (SUSO) SUOMEN SOKERI OY. Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; 08-NOV-1990 (first entry) Base substituted E.coli beta-galactosidase alpha-fragment. Score 41; DB 1; Length 204; Pred. No. 1.18e-10; Introducing random point mutations into nucleic acods misincorporation, completion of molecules and screening 47 C; 17 G; occurred singularly in any given mutant. Location/Qualifiers /function=multiple cloning site LT 6 N81164 standard; DNA; 204 BP. 204 BP; 21 A; Match 2.8%; Local Similarity 10.0%; 11; Conservative 187..204 03-APR-1987; US-034819. Disclosure; p; English. 19..69 30-MAR-1988; 105163. WPI; 88-279927/40. Escherichia coli. See also P80575. misc feature EP-285123-A. 05-MAY-1988. primer bind /*tag= a Sequence Query Match /*tag= Matches g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 tggccctttgggaccttcttctgcaagctcagcagctacctcatcttcgtcaacatgtac 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 TGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCCATCATTGTCCTCAACATGTTT 321
                                                                                                                                                                                                                                                                                                                                                                           partial sequence of the R20 seven transmembrane coding sequence which was later used as a probe for isolating this R20 genomic clone from a human placenta DNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 30; Indels 0; Gaps
                                                              Primer; seven transmembrane receptor; receptor; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer; seven transmembrane receptor; receptor; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                             PCR using two primers (Q66174, Q66175) was performed to amplify a
                                                                                                                                                                                                                                                                                                            prods. for use as therapeutic or diagnostic agents for conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prods. for use as therapeutic or diagnostic agents for conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding seven trans:membrane receptors - used to develop
                                                                                                                                                                                                                                                                                             DNA encoding seven trans:membrane receptors - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                            456 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 40; DB 11; Length 1872;
Best Local Similarity 70.0%; Pred. No. 4.74e-10;
                                                Seven transmembrane receptor (R20) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           491 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seven transmembrane receptor (R2) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 gecagegtettetgeeteaceggeeteagettegaeeget 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 GGCAGTGTTCTGCTTACTGCCATTAGCCTGGATGGCT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= Seven transmembrane receptor (R2) W09412635-A.
                                                                                                                                              /product= R20 Seven transmembrane receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                           592 C;
                                                                                                                                                                                                                                                                                                                                           Example 9; Page 72-74; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godiska R, Gray PW, Schweickart VL;
WPI; 94-200264/24.
                                                                                                                                                                                                                                          Godiska R, Gray PW, Schweickart VL; WPI; 94-200264/24.
                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           328 A;
Q66176 standard; DNA; 1872 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q66177 standard; DNA; 2098 BP
                            06-FEB-1995 (first entry)
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                                                                                                              202..1344
                                                                                                                                                                            09-JUN-1994.
17-NOV-1993; U11153.
17-NOV-1992; US-977452.
(ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                             involving the receptors.
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17-NOV-1993; U11153.
17-NOV-1992; US-977452.
                                                                                                                                                                                                                                                                                                                                                                                                                           1872 BP;
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                                                                                 Homo sapiens.
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                                                                                                                                                             WO9412635-A.
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involving the receptors.

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ö This generic formula can be represented as follows: X(TGC) (NNB)10-(TGC) (NNB)62 (NNB) 2(TGC) (NNB)14 (TGC)Y. X and Y are flanking restriction 981 tggcccgccctttgtgtcccagaagctacgcaccaaggcgatggccggcgggggggtgctgg 1040 Q70469 is a generic DNA sequence used to generate random TSAR peptide 921 tcagcatgtacgccagcgtcctgcttatcacggccatgagtctagaccgctcactggcgg 980 311 TCAACATGTTTGGCAGTGTCTTCCTGCTTACTGCCATTAGCCTGGATCGCTGTTGTGG 370 of the ROY of gene, two weakly hybridising sequences were identified which had significant homology to other seven transmembrane receptors. The probe was used to screen a human genomic foetal liver DNA library, and while the R20 gene could not be identified in putil library, several weakly hybridising clones were plaque purified, subcloned and sequenced. The two clones were designated R2 and R12 ((066178). This is the coding sequence of the R2 clone. Sequence 2098 BP; 371 A; 594 C; 671 G; 462 T; TSAR; totally synthetic affinity reagent; synthetic; binding domain; 0; Mismatches 67; Indels 0; Gaps sites (X is not the same as Y) that are not specified further. This partial sequence of the R20 seven transmembrane coding sequence which was later used as a probe for isolating the R20 genomic clone (Q66176) from a human placenta DNA library. During the isolation sequence generates peptides that are cloverleaf in structure. Other Example 10; Page 75-77; 100pp; English. PCR using two primers (Q66174, Q66175) was performed to amplify a screening a recombinant vector library expressing fusion proteins effector domain; concateneated heterofunctional protein; linker; Generic DNA sequence to generate a random TSAR peptide library. 1041 caggcatctgggtgttgtcctttctgctggccacacccgtcctcgcgtaccg 1092 431 GATGTATCTGGGTGGTGGCTTTTGTGTTGTGCATTCCTGTGTTCGTGTACCG 482 direct; rapid; detection; screening; treatment; generic; ss. Identifying proteins or peptide(s) which bind a ligand - by Query Match 2.6%; Score 38; DB 11; Length 2098; Best Local Similarity 61.0%; Pred. No. 7.38e-09; Matches 105; Conservative 0; Mismatches 67; Indels (comprising a binding domain and an effector domain Disclosure, Page 35; 255pp; English. /*tag= a /note= *this sequence represents '2'; 2 can be a sequence of 6,9 or 12 nucleotides (see Location/Qualifiers Q70469 standard; DNA; 114 BP. 31-JAN-1994; US-189331. (UYNC-) UNIV NORTH CAROLINA. 07-APR-1995 (first entry) 01-FEB-1993; US-013416. 30-DEC-1993; US-176500 Kay BK; 01-FEB-1994; U00977. Fowlkes DM, Kay B WPI; 94-279739/34. = = = misc feature WO9418318-A. 18-AUG-1994. comments) * Synthetic. X S S S S S S S S S S S S S S S S 염 ð g 음 ð ð

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Synthetic Affinity Reagents) peptides. This generic formula can also be Q70470 is a generic DNA sequence used to generate random TSAR (Totally screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 36; 255pp; English. direct; rapid; detection; screening; treatment; generic; ss. Identifying proteins or peptide(s) which bind a ligand - by /*tag= a /note= "encoded by Z (see comments)" Location/Qualifiers (UYNC-) UNIV NORTH CAROLINA. 01-FEB-1994; U00977. 01-FEB-1993; US-013416. 30-DEC-1993; US-176500 55..60 US-189331 EX: WPI; 94-279739/34. P-PSDB; R58378 misc feature 409418318-A. 31-JAN-1994; 18-AUG-1994 Fowlkes DM, Synthetic. Sequence Query Match 070470; Matches 음 ð 셤 ð ID DET DET DE PET DE PE conformational rigidity to the peptides. The TSARs or compsns. comprising concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and ö active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies Synthetic Affinity Reagents) peptides. This generic formula can also be Q70465 is a generic DNA sequence used to generate random TSAR (Totally generated by these generic sequences are shown in R65150-54. TSARs are 146 GCCTGAAGATGCAGCGGACAGTGAACACAATTTGGTTCCTCCACCTCACCTTGGCGGACC 205 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; a second effector peptide portion that is chemically or biologically a TSAR binding domain can be used in vivo to deliver a chemically or 2 gennbnnbnnbnnbnnbnnbnnbnnbnnbtgennbnnbnnbnnbnnbnnbnnbnnnnnn 61 Gaps and therefore circumvent the need for complex methods of hybridoma characterised and have designed activity allowing direct and rapid Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English. generic sequences are shown in Q70465-68. Other specific peptides effector domain; concateneated heterofunctional protein; linker; formation or in vivo antibody production. The TSARs are easily 30; Mismatches 73; Indels 0; direct; rapid; detection; screening; treatment; generic; ss. 206 TCCTCTGCTGCCTTGTCGCTTGCTCGCTCGCTCTCCAG 255 2.4%; Score 34; DB 12; Length 114; 4 T; Pred. No. 1.57e-06; /note= "this sequence represents 'Z'; Z can be 4 G; 9 or 12 nucleotides (see 4 C; Location/Qualifiers detection in a screening process. Sequence 114 BP; 0 A; 4 C Q70465 standard; DNA; 114 BP. 31-JAN-1994; US-189331. (UYNC-) UNIV NORTH CAROLINA. 6.4%; P-PSDB; R65150 and R65151. 05-APR-1995 (first entry) 7; Conservative us-176500. US-013416. 55..60 Kay BK; Best Local Similarity 01-FEB-1994; U00977. WPI; 94-279739/34 sequence of 6, misc feature 30-DEC-1993; 01-FEB-1993; Fowlkes DM, WO9418318-A. 18-AUG-1994 Synthetic. comments) " /*tag= a Sequence Query Match 070465; Matches

쇰 ð 셤 à not specified further. Other generic sequences are shown in Q10466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, ö confer some degree of conformational rigidity to the peptides. The TSARs deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the and Y are flanking restriction sites (X is not the same as Y) that are peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need 120 CAATGGCCTGGTGCTGGCTGGCTGGCCTGAAGATGCAGCGGACAGTGAACACAATTTG 179 Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; Gaps chemically or biologically active. They may further comprise a linker in, or flanking, the unpredicted or variant residues. These residues activity allowing direct and rapid detection in a screening process. Semience 114 BP: 0 A: 2 C; 2 G; 2 T; or compsns. comprising a TSAR binding domain can be used in vivo to comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is as follows: X (NNB) 6 (TGC) (NNB) 112 (NNB) 14 (TGC) (NNB) 3Y. X production. The TSARs are easily characterised and have designed for complex methods of hybridoma formation or in vivo antibody ö 180 GTTCCTCCACCTCACCTTGGCGGACCTCCTCTGCTGCCTCTTGGCCTTC 231 2.4%; Score 34; DB 12; Length 114; 33; Mismatches 75; Indels Pred. No. 1.57e-06; 2 C; Q70470 standard; DNA; 114 BP 0 A; .0-APR-1995 (first entry) Best Local Similarity 3.6%; 4; Conservative 88888888888888888888888888

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-(CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same
                                                                                                                heterofunctional proteins or peptides, comprising at least two functional regions – a binding domain with affinity for a ligand and a second
                                            as Y) that are not specified further. The peptides generated by this and other generic sequences (Q70471-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated
                                                                                                                                                            effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the
as follows: X (NNB) 4 (CAC) (NNB) 4 (CAC) (NNB) 8Z (NNB) 6 (CAC) (NNB) 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70467 is a generic DNA sequence used to generate random TSAR (Totally
                                                                                                                                                                                                                                                                                                            monoclonal or polyclonal antibodies and therefore circumvent the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 TTGGTTCCTCCACCTCACCTTGGCGGACCTCCTCTGCTGCTCCTTCGCTTCTCGCT 236
                                                                                                                                                                                                                                                                                                                                                        production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 5 A; 10 C; 0 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches 67; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            effector domain; concateneated heterofunctional protein; linker;
                                                                                                                                                                                                                                                                                 cell. They can also replace the function of macromolecules, eq.
                                                                                                                                                                                                                                                                                                                                    for complex methods of hybridoma formation or in vivo antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 34; DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 bnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbc 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 GCTCACTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCC 280
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/note= "this sequence represents '2'; Z can be a
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WPI; 94-279739/34.
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  represented
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonnal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoms formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing confer some degree of conformational rigidity to the peptides. The TSARs and Y are flanking restriction sites (X is not the same as Y) that are peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned chemically or biologically active. They may further comprise a linker in, or flanking, the unpredicted or variant residues. These residues or compsns. comprising a TSAR binding domain can be used in vivo to comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is deliver a chemically or biologically active moiety, eg. metal ion, Length 114; direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T; Query Match 8888888888888888888888888

Gaps ; ; 33; Mismatches 75; Indels 2.4%; Score 34; DB 12; I 3.6%; Pred. No. 1.57e-06; Best Local Similarity 3.6%; 4; Conservative Matches

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225 GGCCTTCTCGCTGGCTCACTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCCTATG 284 쇰 à

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285 CAAGCTCATCCCTCCATCATTGTCCTCAACATGTTTGGCAGTGTCTTCCTG 336

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Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Q70468 standard; DNA; 114 BP 05-APR-1995 (first entry)

/*tag= a /note= "this sequence represents $^{\prime}2'$; $^{\prime}2$ can be a sequence of 6, 9 or 12 nucleotides (see Location/Qualifiers misc feature Synthetic.

(UYNC-) UNIV NORTH CAROLINA. 01-FEB-1993; US-013416. 30-DEC-1993; US-176500. 31-JAN-1994; US-189331. 01-FEB-1994; U00977. W09418318-A 18-AUG-1994 Fowlkes DM, comments) "

screening a recombinant vector library expressing fusion proteins Identifying proteins or peptide(s) which bind a ligand - by WPI; 94-279739/34. P-PSDB; R65154.

comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English. Q70468 is a generic DNA sequence used to generate random TSAR (Totally

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Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions — a binding domain with affinity for a ligand and a second effector peptide portion that is production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. ö confer some degree of conformational rigidity to the peptides. The TSARs deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the and Y are flanking restriction sites (X is not the same as Y) that are that the expressed peptide contains 2 or 4 cysteine residues positioned peptide between the 2 domains. The oligonucleotides are also designed so Synthetic Affinity Reagents) peptides. This generic formula can also be not specified further. Other generic sequences are shown in Q70466-68. cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody 183 CCTCCACCTCACCTTGGCGGACCTCCTCTGCTGCCTTGGCCTTCTCGCTGGCTCA 242 chemically or biologically active They may further comprise a linker 3 banbanbanbanbanbanbanbanbanbanbtgcnnbanbanbanbanbanbannnnnn 62 Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; or flanking, the unpredicted or variant residues. These residues or compsns. comprising a TSAR binding domain can be used in vivo to represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English. ö 63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114 243 CTTGGCTCTCCAGGGACAGTGGCCCTACGCCAGGTTCCTATGCAAGCTCATC 294 direct; rapid; detection; screening; treatment; generic; ss. Identifying proteins or peptide(s) which bind a ligand - by Score 34; DB 12; Length 114; 32; Mismatches 75; Indels /*tag= a
/note= *this sequence represents '2'; 2 can be a Pred. No. 1.57e-06; sequence of 6,9 or 12 nucleotides (see Location/Qualifiers Q70469 standard; DNA; 114 BP. (UYNC-) UNIV NORTH CAROLINA. Best Local Similarity 4.5%; 5; Conservative 07-APR-1995 (first entry) US-013416. US-176500. 01-FEB-1994; U00977. 01-FEB-1993; US-013416. 30-DEC-1993; US-176500. 31-JAN-1994; US-189331. 55..60 Kay BK; WPI; 94-279739/34. misc feature WO9418318-A. 18-AUG-1994. Fowlkes DM, Synthetic. comments) Sequence Query Match 070469; Matches 'n, RESULT 888888888888888888888888888 쇰 셤 8 ð

conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and ö This generic formula can be represented as follows: X(TGC) (NNB)10-(TGC) (NNB)62 (NNB)2 (TGC) (NNB)14 (TGC)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This sequence generates perties that are cloverleaf in structure. Other generic sequences are shown in Q70465-68. Other specific peptides generated by these generic sequences are shown in R65150-54. TSARs are active.They may further comprise a linker peptide between the 2 domains. biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of Q70469 is a generic DNA sequence used to generate random TSAR peptide 235 GCGAGAAGGCCAAGGAGGCGAGCAGGAGGTCCGCCAAGGTGAGGAGGAACCAAA 176 The oligonucleotides are also designed so that the expressed peptide Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; a second effector peptide portion that is chemically or biologically 2 gcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnn 61 Gaps characterised and have designed activity allowing direct and rapid concateneated heterofunctional protein; linker; Cormation or in vivo antibody production. The TSARs are easily ö direct; rapid; detection; screening; treatment; generic; ss. Identifying proteins or peptide(s) which bind a ligand - by Length 114; 31; Mismatches 73; Indels 4 T; /note= "this sequence represents 'Z'; Z can be a Pred. No. 1.57e-06; Score 34; DB 12; 4 G; sequence of 6, 9 or 12 nucleotides (see Location/Qualifiers 4 C; detection in a screening process. Q70465 standard; DNA; 114 BP (UYNC-) UNIV NORTH CAROLINA 2.4%; 0 A; 5.5%; 05-APR-1995 (first entry) P-PSDB; R65150 and R65151. 6; Conservative 01-FEB-1993; US-013416. US-176500 31-JAN-1994; US-189331. 55..60 Kay BK; 01-FEB-1994; U00977. Best Local Similarity WPI; 94-279739/34. effector domain; misc feature WO9418318-A. 18-AUG-1994. 30-DEC-1993; Fowlkes DM, comments) " Synthetic. Sequence /*tag= a Query Match 070465; Matches 음 g, g გ

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not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. R65151-54. TSARs are concatenated heterofunctional proteins or peptides, and Y are flanking restriction sites (X is not the same as Y) that are screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure, Page 35; 255pp; English. 970465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB) 6(TGC) (NNB) 112 (NNB) 14 (TGC) (NNB) 3Y, X monoclonal or polyclonal antibodies and therefore circumvent the need activity allowing direct and rapid detection in a screening process. Sequence 114 BP: 0 A; 2 C; 2 G; 2 T; comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is production. The TSARs are easily characterised and have designed for complex methods of hybridoma formation or in vivo antibody

Query Match 2.4%; Score 34; DB 12; Length 114; Best Local Similarity 4.5%; Pred. No. 1.57e-06; Matches 5; Conservative 32; Mismatches 75; Indels 0; Gaps

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63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnb 114

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198 CAAGGTGAGGTGGAGGAACCAAATTGTGTTCACTGTCGGCTGCATCTTCAGG 147

Search completed: Wed May 1 16:38:05 1996 Job time : 118 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed May 1 15:29:30 1996; MasPar time 19.61 Seconds 621.257 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score: Title:

>US-08-462-355-2 (1-482) from USO8462355.pep 3591 1 MASFSAETHNSTDLLSQPWNE.....TRSTHCPSNNVISERNSTTV 482 Sequence:

PAM 150 Gap 11 Scoring table:

82306 seqs, 25270970 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir46 Database:

1:annl 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2

Mean 48.219; Variance 119.102; scale 0.405 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.01e-73	2.58e-70	3.74e-70	2.84e - 66	5.98e-66	3.28e-63	1.92e-61	8.44e - 61	9.42e-48	1.31e-44	7.84e-37	1,90e-35
Description	complement C5a recep	complement C5a anaph	FMLP-related recepto	C5a anaphylatoxin re	FMLP-related recepto	N-formyl peptide che	N-formyl peptide rec	N-formyl peptide rec	G protein-coupled re	G protein-coupled re	angiotensin II recep	andiotensin II recep
ID	527357	A37963	B42009	A46525	C42009	A49542	A46520	A42009	JC2492	A55733	JN0694	544425
DB	11	10	10	11	10	11	11	10	11	10	10	13
* Query Match Length DB	352	320	351	351	353	364	352	320	353	355	362	359
% Query Match	16.7	16.2	16.1	15.5	15.4	14.9	14.6	14.5	12.2	11.7	10.3	10.0
Score	601	580	579	555	553	536	525	521	439	419	369	360
Result No.	-	2	e	4	5	9	7	œ	9	10	II	12

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1.90e - 35	5.50e-35	5.50e-35	7.83e - 35	1.11e - 34	3.21e - 34	3.21e-34	6.50e-34	2.66e-33	2.19e - 32	2.19e-32	2.19e - 32	1.54e - 32	4.41e - 32	4.41e - 32	4.41e-32	4.41e-32	1.26e - 31	1.26e - 31	3.60e - 31	5.11e-31	3.60e - 31	4.14e-30	1.46e - 30	5.87e-30	1.67e - 29	1.34e - 28	1.34e - 28	٠.	5.35e-28	3.01e-27	4.24e-27	9.36e-26	
angiotensin II recep	type-1 angiotensin I	angiotensin II recep	11	angiotensin II recep	angiotensin II recep	angiotensin II recep	AT1 angiotensin II r	angiotensin receptor	leukocyte-derived se	receptor D2S201E - h	neuropeptide Y recep	angiotensin II recep	Ξ	angiotensin receptor	angiotensin II recep	Angiotensin II recep	interleukin-8 recept	interleukin-8 recept	neuropeptide Y recep	interleukin-8 recept	angiotensin II recep	interleukin-8 recept	angiotensin II recep	bradykinin receptor	angiotensin II recep	somatostatin recepto	somatostatin recepto	probable G protein-c	somatostatin recepto	opioid receptor - ra	mu opiate receptor -	interleukin-8 recept	
JC1194	A44014	JC1104	\$15403	JH0578	A42656	520423	A48857	JH0622	A53103	A45747	532761	JQ1516	JC2134	JH0621	S20424	S15404	A53611	A39446	528787	JQ1231	JC1193	A39445	JQ1055	A53858	PN0449	A46226	\$32501	S30508	A44021	S34593	S41075	A23669	
Ξ	11	10	13	11	11	13	11	11	10	11	10	1	11	Ξ	13	13	10	10	11	11	11	10	11	10	10	Ξ	13	11	11	13	13	Ξ	
329	359	329	329	329	329	359	359	359	352	352	352	359	359	359	359	359	355	355	353	355	359	350	329	353	238	418	418	428	428	398	400	354	
10.0	9.6	6.6	6.6	6.6	8.6	8.6	9.1	9.6	9.5	9.5	9.5	9.5	9.4	9.4	9.4	9.4	9.3	9.3	9.5	9.5	9.5	9.1	9.1	9.0	8.9	œ œ	8.8	8.7	8.7	8.5	8.5	8.2	
360	357	357	356	355	352	352	320	346	340	340	340	341	338	338	338	338	335	335	332	331	332	325	328	324	321	315	315	312	311	306	305	296	
13	14	15	16	17	18	19	70	21	22	23	54	52	36	27	88	59	30	31	35	33	34	35	36	37	38	33	40	41	42	43	44	45	

ALI GNMENTS

RESULT

#type complete	complement C5a receptor - dog	fformal_name Canis lupus familiaris fcommon_name dog	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change				Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.	Biochem. J. (1992) 288:911-917	Cloning and functional expression of the canine anaphylatoxin	C5a receptor. Evidence for high interspecies variability.		ıry		label PER	09859)	#length 352 #molecular-weight 39212 #checksum 9479		: Pred. No. 1.01e-73; 53; Mismatches 40; Indels 0; Gaps 0;
\$27357 #ty	complement C5a	#formal_name C	13-Jan-1995 #s	13-Jail-1993	S27357	\$27357	Perret, J.J.;	Biochem. J. (1	Cloning and fu	C5a receptor	527357	preliminary	##molecule type mRNA	s 1-352 ##label PER	##cross-references EMBL:X65860	#length 352 #	16.7%;	<pre>Best Local Similarity 43.3%; Matches 71; Conservative</pre>
ENTRY	TITLE	ORGANISM	DATE		ACCESSIONS	REFERENCE	#authors	# journal	#title		#accession	##status	##molecn]	##residues	##cross-re	SUMMARY	Query Match	Best Local Sin Matches 71,

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FMLP receptor (FPR), and two FMLP receptor homologue orphan nucleotide sequence is not given; authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 as Thr, and GGC for residues 264 as Ala; translation for residue 265 was not shown This G-protein coupled receptor, homologous to the N-formyl peptide Isolation of a cDNA that encodes a novel granulocyte N-formyl receptor FPR1, does not bind prototype N-formyl peptide ligands (reference A42492, but see also JQ1521). It is expressed only on differentiated myeloid cells and is probably a chemotactic Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochrane, C.G. Cloning of a cDNA encoding a receptor related to the formyl Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, Mapping of genes for the human C5a receptor (C5AR), human Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews A structural homologue of the N-formyl peptide receptor. Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change Characterization and chromosome mapping of a peptide Biochem. Biophys. Res. Commun. (1992) 184:582-589 receptors (FPRH1, FPRH2) to chromosome 19. sequence extracted from NCBI backbone peptide receptor of human neutrophils B42009; JC1258; JQ1521; A42492; S21581 nucleotide sequence is not given J. Biol. Chem. (1992) 267:7637-7643 chemoattractant receptor family. ##cross-references NCBIN:94159; NCBIP:94160 McDermott, D.; Francke, U. #fexperimental_source bone marrow mRNA Genomics (1992) 13:437-440 Gene (1992) 118:303-304 1-351 ##label MUR 1-351 ##label PER 1-351 ##label YE2 ##cross-references EMBL:X63819 peptide receptor. fMet-Leu-Phe tcross-references MUID:92218423 fcross-references MUID:92380523 cross-references MUID:92246937 ##cross-references GB:M88107 14-Jul-1995 ##molecule type mRNA ##molecule_type mRNA ##molecule_type mRNA ##molecule_type DNA A42009 JC1258 B42009 JQ1521 A42492 JQ1521 #residues ##residues ##residues accession #accession *accession #accession #note ##note #note authors f journal *authors authors #authors #journal # journal iournal ACCESSIONS title title REFERENCE title REFERENCE title REFERENCE REFERENCE COMMENT DATE

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#authors # journal **ACCESSIONS** 120 Matches REFERENCE title GENETICS # dene ORGANISM KEYWORDS COMMENT SUMMARY RESULT RESULT TITLE ENTRY g a ð 쇰 ð 셤 à ò 음 g ð ð 1; peptidergic G-protein-coupled receptors. Molecular cloning #fetatus preliminary; not compared with conceptual translation #fmolecule_type nucleic acid 87 mgekwpfgwflcklihivvdinlfgsvfligfialdrcicvlhpvwagnhrtvslamkvi 146 84 LQGQWPYGRFLCKLIPSIIVINMFGSVFLLTAISLDRCLVVFKPIWCQNHRNVGMACSIC 143 #domain transmembrane #status predicted #label TRIN #domain transmembrane #status predicted #label TIIN #domain transmembrane #status predicted #label IIIN #domain transmembrane #status predicted #label TIIN #domain transmembrane #status predicted #label TVN #domain transmembrane #status predicted #label TVN 24 ILSHVILSLIFELGLPGNGLVIÄVAGIKMORTVNTIÄFEHLTLADLICCISLAFSLAHLA 83 #domain transmembrane #status predicted #label TVIN #domain transmembrane #status predicted #label VIIN 27 ilplvvlgvtfvlgvlgnglviwvagfrmtrtvtticylnlaladfsftatlpflivsma 86 #binding site carbohydrate (Asn) (covalent) #status Gaps 18-Jun-1993 #sequence revision 18-Nov-1994 #text_change <u>-</u> #length 351 #molecular-weight 38954 #checksum 5965 #length 351 #molecular-weight 38964 #checksum 3402 Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, formal name Mus musculus fcommon name house mouse Structural diversity in the extracellular faces of 43; Mismatches 39; Indels 1; chemotaxis response; G protein-coupled receptor; 15.5%; Score 555; DB 11; Length 351; 42.9%; Pred. No. 2.84e-66; Length 351; C5a anaphylatoxin receptor, C5aR=peptidergic sequence extracted from NCBI backbone of the mouse C5a anaphylatoxin receptor. #cross-references MUID:93017861 fdisulfide_bonds fstatus predicted glycoprotein; transmembrane protein G-protein-coupled receptor - mouse Score 579; DB 10; Pred. No. 3.74e-70; J. Immunol. (1992) 149:2600-2606 144 GCIWVVAFVLCIPVFVYREIFTTDNHNR-CGYKFG 177 147 vgpwilalvltlpvflflttvtipngdtyctfnfa 181 Query Match 16.1%; Score 579; Best Local Similarity 46.5%; Pred. No. 3 Matches 72; Conservative 43; Mismat. receptor for some other ligand #type complete 1-351 ##label GER ##cross-references NCBIP:116075 ##experimental_source BALB/C predicted\ status absent 28-Apr-1995 Gerard, N.P. fmap_position 19q13.3-q13.4 GDB:FPRL1 Best Local Similarity A46525 A46525 A46525 ##residues faccession Query Match #note #authors #journal #introns 242-266 282-307 ACCESS IONS 145-169 206-226 100-121 REFERENCE 98-176 #title FEATURE 27-53 #gene 59-83 ORGANISM KEYWORDS GENETICS SUMMARY SUMMARY RFSULT TITLE ENTRY 쇰 g g ò

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Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19. C42009 FMLP-related receptor 2 - human FMLP-related receptor FPRH2 #MLP-related receptor I; probable chemotactic receptor FPRH2 #formal name Homo sapiens #common_name man 1.5ep-1993 #sequence_revision 30-Sep-1993 #text_change 14-Jul-1995 ä This iMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears not to expressed in neutrophils. Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, 63 cylnlaladfsfsailpfrmvsvamrekwpfasflcklvhvmidinlfvsvylitiiald 122 123 rcicvlhpawaqnhrtmslakrvmtglwiftivltlpnfiiwttisttngdtycifnfaf 182 91 vlfttvlnhnywyfdatacivlpslillnmyasilllatisadrfllvfkpiwcqkvrgt 150 RCLVVFKPIWCQNHRNVGMACSICGCIWVVAFVLCIPVFVYRE-IFTTDNHNRCGYKFGL 178 17 PWNEPPVILSHVILSLYFFLGLEGRGKLYLWYGKKWQRTWYTHFLHLTLADLLCCLSLA 76 3 tnfsiplneteevlpepaghtvlwifsllvhgvtfvfgvlgnglviwvagfrmtrtvnti 62 2 ASFSAETNSTD-LLSQPWNEPPV-ILSMVILSLFFLLGLPGNGLVLWVAGLKMQRTVNTI 59 8 Gaps Gaps 31 pkrqpgdvaaliiysvvflvgvpgnalvvwvtafepdgpsnaiwflnlavadllsclamp glycoprotein; transmembrane protein #length 353 #molecular-weight 40015 #checksum 8135 3; 2 chemotaxis response; G protein-coupled receptor; Score 553; DB 10; Length 353; Pred. No. 5.98e-66; 56; Mismatches 49; Indels Indels 151 glawmacgvawvlallltipsfvyreaykdfysehtvcginyg 193 nucleotide sequence is not given 46; Mismatches 45; Genomics (1992) 13:437-440 type complete #type complete 1-353 ##label BA0 ##cross-references GB:M76673 15.4%; Query Match
Best Local Similarity 40.0%;
watches 72; Conservative #status absent Conservative #map position 19q13.3-q13.4 GDB: FPRL2 ##molecule_type DNA A49542 A42009 C42009 C42009 70; ##residues ALTERNATE NAMES #accession #note 9 ഹ introns ENTRY

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Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P. Biochemistry (1990) 29:11123-11133 The human N-formylpeptide receptor. Characterization of two Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P. Biochem. Biophys. Res. Commun. (1990) 168:1103-1109 Synthesis and use of a novel N-formyl peptide derivative to isolate a human N-formyl peptide receptor cDNA. Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, ##molecule_type DNA ##residues 1,'G',3-28,30-100,'L',102-104,106-112,'FLIA',115-176, 87 lgghwpfgwflckfvftivdinlfgsvflialialdrcicvlhpvwagnhrnvslakkvi 146 24 ILSMVILSLTFLIGLPGNGLVLMVAGLKMQRTVNTIMFLHLTTADLLCCLSLAFSLAHLA 83 27 vfsylilvvtfvlgvlgnglviwvtgfrmthtvttisylnlaladfsftstlpffivtka 86 Gaps #formal name Homo sapiens #common_name man
30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K. Gene (1993) 133:285-290 Sequence and organization of the human N-formyl peptide cDNA isolates and evidence for a new subfamily of .; ##molecule_type mRNA ##residues 1-191,'N',193-345,'E',347-350 ##label BOU not compared with conceptual translation not compared with conceptual translation Indels receptors (FPRH1, FPRH2) to chromosome 19. A42009 I-100, 'L', 102-191, 'N', 193-350 ##label 44; Mismatches 31; A42009 #type complete N-formyl peptide receptor - human G-protein-coupled receptors. #cross-references MUID:91105045 JC2014; A36309; A35495; A42009 192-Asn was also found Genomics (1992) 13:437-440 Conservative 5; Matches

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SUMMARY SUMMARY RESULT ENTRY 330 RESULT ENTRY TITLE DATE 쇰 쇰 g ð g à 셤 õ 유 ð ð ð 5 Mapping studies of two G protein-coupled receptor genes: An amino acid difference may confer a functional variation Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, Goodman, M.; George, S.R.; O'Dowd, B.F. Biochem. Biophys. Res. Commun. (1994) 205:1952-1958 !binding_site phosphate (Thr) (covalent) (by protein 86 amgghwpfgwflckfvftivdinlfgsvflialialdrcvcvlhpvwtqnhrtvslakkv 145 24 ILSHVILSLYFELGLPGNGLVLMVAGIKMQRTVNTIWFLHLTLADLLCCLS-LAFSLAHL 82 TM6\ 27 iitylvfavtfvlgvlgnglviwvagfrmthtvttisylnlavadf-cftstlpffmvrk 85 fdomain transmembrane #status predicted #label TM1\
fdomain transmembrane #status predicted #label TM2\
fdomain transmembrane #status predicted #label TM3\ #domain transmembrane #status predicted #label TM3\
#region DR motif\
#domain transmembrane #status predicted #label TM4\
#domain transmembrane #status predicted #label TM5\ binding_site carbohydrate (Asn) (covalent) #status domain transmembrane #status predicted #label TM7 #binding site carbohydrate (Asn) (covalent) #status Gaps #formal name Rattus norvegicus #common name Norway rat 16-Mar-1995 #sequence_revision 26-May-1995 #text_change entire coding region is found in exon 3; alternatively 178-182, 184-191, 'N', 194-248, 250-267, 270-329, 'E' spliced mRNA transcripts include or exclude exon 2 predicted #length 350 #molecular-weight 38401 #checksum 5503 domain transmembrane #status predicted #label **5**; chemotaxis response; G protein-coupled receptor; Query Match 14.5%; Score 521; DB 10; Length 350; Best Local Similarity 46.7%; Pred. No. 8.44e-61; 46; Mismatches 25; Indels glycoprotein; membrane protein; receptor between a human and rodent receptor. glycoprotein; transmembrane protein nucleotide sequence is not given G protein-coupled receptor 1 - rat 331-350 ##label BAO #type complete 1-353 ##label MAR predicted\ ||:|::| :||:: | 143 CGCIWVVAFVLCIPVFV 159 #status absent 146 iigpwvmallltlpvii 162 64; Conservative 26-May-1995 ##molecule_type mRNA 19q13.4 JC2492 GPR-1 fmap_position fintrons # residues ALTERNATE NAMES FEATURE 69-135 74-94 112-133 134-135 155-175 209-229 246-266 246-266 #accession ##note #authors # journal 150, 231 **ACCESSIONS** 14, 273 REFERENCE #title #dene #note GENETICS ORGANISM KEYWORDS KEYWORDS FEATURE SUMMARY RESULT ENTRY

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ï Ë Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.C.; Shi, X.; George, S.R.; O'Dowd, B.F. 100 nfhwpfgiwlckansftaqlnmfasvffltvisldhyihlihpvlshrhrtlknslivii 159 100 sfhwpfgrwlcklnsfiaglnmfssvffltvisldryihlihpglshphrtlknsllvvl 159 40 vslvlyclafvlgipgnaiviwftglkwkktvttlwflnlaiadfifllflplyisyvam 99 40 islllyalafvlgipgnaiviwfmgfkwkktvttlwflnlaiadfifvlflplyisyval 99 25 LSMVILSLTFLLGLPGNGLVLWVAGIKMQRTVNTIWFLHLTLADLLCCLSLAFSLAHLAL 84 Gaps Gaps #formal name Homo sapiens #common name man
07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
07-Jul-1995
A55733 Cloning of human genes encoding novel G protein-coupled #binding_site palmitate (Cys) (covalent) #status #length 355 #molecular-weight 41396 #checksum 803 46; Mismatches 47; Indels 1; 46; Mismatches 45; Indels 1; predicted #length 353 #molecular-weight 40901 #checksum Score 419; DB 10; Length 355; Pred. No. 1.31e-44; Query Match 12.2%; Score 439; DB 11; Length 353; Best Local Similarity 39.1%; Pred. No. 9.42e-48; protein-coupled receptor GPR1 - human kinase A) #status predicted\ 160 fvwllasllggptlyfrdtvevnnriic-yn 189 160 fiwllasliggpalyfrdtvefnnhtlc-yn 189 145 CIWVVAFVLCIPVFVYREIFTTDNHNRCGYK 175 Genomics (1994) 23:609-618 #type complete ##residues 1-355 ##label MAR ##cross-references GB:U13666 preliminary Query Match 11.7%; Best Local Similarity 37.7%; Matches 57; Conservative 59; Conservative receptors. A55733 #molecule_type DNA A55733 ##status #accession 10 #authors 🕯 journal ACCESS IONS #title Matches REFERENCE ORGANISM gene GENETICS

#type complete

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DATE	REFERENCE #authors	<pre># journal #title</pre>	#accession	##resi SUMMARY	Query Matc	Matches	Db 27 if	Qy 24 IL	Db 86 vy	Qy 80 AH	Db 146 kv	Qy 140 CS		RESULT 13 ENTRY	TITLE ORGANISM DATE	31100	ACCESSIONS REFERENCE	4	# Journal # title	#Cross-re #accessio	##mole ##resi	FEATURE 30-53 65-90	103-123	195-218 240-263 278-300	4,176,188	Query Matc Best Local
TITLE angiotensin II receptor - African clawed irog ORGANISM #formal_name Xenopus laevis #common_name African clawed frog DATE 03-Feb-1994 #secuence revision 03-Feb-1994 #text chance	25-Aug-1995 - 25	July H.; Sandberg, K.; Zhang, Y.; Catt, K.J. Blochen. Blophys. Res. Commun. (1993) 194:756-762 Molecular Standard Commencing and Structural Commen	sion	<pre>##molecule_type_mRNA ##residues 1-362 ##label JIH ##rrose_reference CB-11462</pre>	##CLOSS-LELECTICS OF LLOYOU REFERENCE \$47627 #anthors Nishimaten, S.: Kowasn, N.: Sngava, T.: Ohnishi, J.:	Yamagishi, T.; Murakami, K.; Miyazaki, H. Biochim, Biochys, Acta (1994) 1218:401-407		receptor.	##status preliminary	morecure_ residues_	glycoprotein; transmembrane proteir		<pre>#domain transmembrane #status predicted #label #domain transmembrane #status predicted #label</pre>	#domain transmembrane #status predicted #label #domain transmembrane #status predicted #label	263-303 fdomain transmembrane fstatus predicted flabel im/\ 3,18,177 fbinding site carbohydrate (Asn) (covalent) fstatus	222,343 #binding_site phosphate (Thr) (covalent) fstatus	predicted) 347 #binding site phosphate (Ser) (covalent) #status predicted	SUMMARY #length 362 #molecular-weight 41293 #checksum 4476	atch 10.3%; Score 369; DB 10; Length 362; cal Similarity 35.6%; Pred. No. 7.84e-37;	Matches 52; Conservative 48; Mismatches 40; Indels 6; Gaps 6;	<pre>Db 28 ifiaipiiystifuvqyfqnsmvviviysymkm-ktvasiflmnlalsdl-cfvitlplw 85 ::::: :: : :: : :: : </pre>	Db 86 aaytamhyhwpfgnflckvastaithnlyttvflltclsidrysaivhpmksriwrtamv 145	Qy 79 LAHLALQGQMPYGRFLCKLIPSIIVLAMFGSVFLLTAISLDRCLVVFKPIWCQNHRNVGM 138	<pre>Db 146 arltcvgiwlvaflasmpsijyrqiy 171</pre>	DECENTA 1.2	X.

.; 6 ä Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, s Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.;
van der Meer-de Jong, R.; Inagami, T.; Ichikawa, I.
l Biochem. Biophys. Res. Commun. (1992) 186:1042-1049
Analysis of the evolution of angiotensin II type 1 receptor
gene in mammals (mouse, rat, bovine and human).
references MUID:92359981 Molecular cloning of the canine angiotensin II receptor. An ATI-like receptor with reduced affinity for DuP753. ytameyrwpfgnylckiasasvsfnlyasvflltclsidryvaivhpmkspvrrtmlma 145 Gaps ch 10.0%; Score 360; DB 13; Length 359; l. Similarity 33.7%; Pred. No. 1.90e-35; 56; Conservative 53; Mismatches 49; Indels 8; Gaps fvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 #binding_site carbohydrate (Asn) (covalent) #status JC1194 #type complete
angiotensin II receptor 1B - mouse
#formal name Mus musculus #common_name house mouse
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 07-Oct-1994 fsequence_revision 07-Oct-1994 ftext_change 07-Oct-1994 preliminary 1-359 ##label BUR #length 359 #molecular-weight 40901 #checksum 3882 #length 359 #molecular-weight 40857 #checksum 3978 .; 8 cch 10.0%; Score 360; DB 11; Length 359; al Similarity 33.7%; Pred. No. 1.90e-35; 56; Conservative 53; Mismatches 49; Indels 8 | ||::| : :| :: |::| || |::| :: |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| vtciiiwllaglaslptiihrnvffientnitvcafhyesqnstl 191 #domain transmembrane #label TM1\
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#domain transmembrane #label TM4\
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#domain transmembrane #label TM6\ nucleotide sequence is not given FEBS Lett. (1994) 343:146-150 1-359 ##label YOS predicted ecule type DNA S44425 idues idues G œ

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27 ifvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 cross-references MUID:92337608 ##residues *residues ##residues accession #accession #accession #accession 145-167 194-216 241-264 281-305 4,176,188 #authors #authors #journal #authors f journal f journal 103-124 #title #title REFERENCE REFERENCE 30-53 65-90 GENETICS # gene FEATURE 셤 ð fauthors Curnow, K.M.; Pascoe, L.; White, P.C.
fjournal Mol. Endocrinol. (1992) 6:1113-1118
ftitle Genetic analysis of the human type-1 angiotensin II receptor.
fcross-references MUID:92375105 Mauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z. Biochem. Biophys. Res. Commun. (1992) 186:277-284 Cloning, expression, and characterization of a gene encoding ÷ 86 vytameyrwpfgnylckiasasvsfnlyasvflltclsidrylaivhpmksrlrrtmlva 145 27 ifvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 27 ifvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 A44014 #type complete
type-1 angiotensin II receptor - human
#formal name Homo sapiens #common name man
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change #formal name Homo sapiens #common name man
09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change ##cross-references NCBIN:111831; NCBIP:111833
##note sequence extracted from NCBI backbone
RY #Length 359 #molecular-weight 41061 #checksum 1836 54; Mismatches 48; Indels 8; Query Match 9.9%; Score 357; DB 11; Length 359; Best Local Similarity 33.7%; Pred. No. 5.50e-35; Matches 56; Conservative 54; Mismatches 48; Indels the human angiotensin II type 1A receptor. 140 CSICGCIWVVAFVICIPVFVYREIFTTDNHN-R-CGYKE-GLSSSL 182 146 kvtciiiwlmaglaslpaviyrnvyfiantnitvcafhyesqnstl 191 146 kvtciiiwllaglaslpaiihrnvffientnitvcafhyesqnstl 191 angiotensin II receptor type 1 - human angiotensin II receptor 1A 23-Mar-1995 JC1104; JQ1402; JH0574; JH0267; S18983 #type complete 1-359 ##label CUR preliminary 04-Dec-1994 ##molecule_type mRNA A44014 JC1104 A44014 ##residues ALTERNATE NAMES accession #status ACCESSIONS REFERENCE #authors #journal
#title ACCESS I ONS TITLE ORGANISM REFERENCE ORGANISM SUMMARY RESULT TITLE ENTRY ENTRY

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Cloning and characterization of a human angiotensin II type 1 Molecular cloning, sequence analysis and expression of a cDNA .; 6 Furuta, H.; Guo, D.F.; Inagami, T. Biochem. Biophys. Res. Commun. (1992) 183:8-13 Molecular cloning and sequencing of the gene encoding human Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; Griffin, E.; Stadel, J.M.; Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, Haji, M.; Inagami, T.; Furuta, H.; Gou, D.F.; Nakamuta, #binding_site carbohydrate (Asn) (covalent) #status predicted glycoprotein; hormone receptor; transmembrane protein #length 359 fmolecular-weight 41061 fchecksum 1836 Query Match 9.9%; Score 357; DB 10; Length 359; Best Local Similarity 33.7%; Pred. No. 5.50e-35; Matches 56; Conservative 54; Mismatches 48; Indels 8; Biochem. Biophys. Res. Commun. (1992) 183:910-916 Aiyar, N. Biochem. Biophys. Res. Commun. (1992) 183:989-995 encoding human type-1 angiotensin II receptor. #domain transmembrane #label TM5\
#domain transmembrane #label TM6\
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#domain transmembrane #label TM3\ #domain transmembrane #label TM4\ #domain transmembrane #label angiotensin II type 1 receptor cession cv-##molecule_type DNA
1-359 ##label MAU 1-359 ##label FUR 1-359 ##label TAK ##experimental source lymphocyte NCE JH0574 ##cross-references EMBL:Z11162 1-359 ##label fcross-references MUID:92181475 #cross-references MUID:92198490 #cross-references MUID:92231907 ##cross-references GB:M87290 ##experimental source liver NCE JH0267 ##experimental_source liver Nawata, H. ##molecule_type mRNA GDB:AGTR1 ##molecule_type mRNA ##molecule_type DNA #map_position 3q21-q25 KEYWORDS alvcopro JH0267 JQ1402 JH0574

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 1 15:28:15 1996; MasPar time 9.52 Seconds 419.333 Million cell updates/sec Run on:

Tabular output not generated.

1 MASFSAETNSTDLLSQPWNE.....TRSTHCPSNNVISERNSTTV 482 >US-08-462-355-2 (1-482) from US08462355.pep 3591 Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

70887 seqs, 8282111 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq22 1:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 Database:

Mean 35.628; Variance 159.312; scale 0.224 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•					
Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description	Pred. No.
-	390	10.9	!	2	i –	Seven transmembrane r	7.17e-24
2	355	9.6		6	_	Human angiotensin II	9.41e-21
٣	340	9.5		10	_	Seven transmembrane r	2.00e-19
4	340	9.5		12		Human monocyte PF4AR.	2.00e-19
2	340	9.5		5	_	New platelet factor 4	2.00e-19
9	335	9.3		-		Human IL-8 receptor f	5.53e-19
1	335	9.3		9		Sequence in a low aff	5.53e-19
00	335	9,3		14		IL8-R type 2-GBP 130	5.53e-19
6	331	9.5		9	_	Sequence in a high af	1.25e-18
10	325	9.1		2	_	Interleukin-8 recepto	4.21e-18
11	325	9.1	350 12	12	R68811	Interleukin-8 recepto	4.21e-18
12	325	9.1		14	_	IL8-R type 1-GBP 130	4.21e-18

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Human somatostatin re	Seven transmembrane r	Murine somatostatin r	Human mu opiate recep	Murine mu-subtype opi	Murine C140 receptor.	Rat mu opiate recepto	Rat mu opioid recepto	Murine C140 receptor	Human mu opioid recep	Epsilon opioid recept	$\overline{}$	Murine somatostatin r	Human somatostatin re	Human C140 receptor	Human C140 receptor.	Seven transmembrane r	Sequence in a lowh af	New platelet factor 4	Human lymphocyte PF4A	Mammalian kappa opioi	Mouse kappa opioid re	Rat kappa opiate rece	Human somatostatin re	Murine somatostatin r	Rat delta opiate rece	Rat opioid receptor.	Mouse opioid receptor	Pituitary somatostati	Murine delta opioid r	Mouse delta opioid re	Sequence of murine de	Partial sequence of s
R39263	R53750	R39264	R76780	R65188	R66920	R76781	R71964	R66922	R71966	R72985	R53932	R39260	R39259	R66923	R66921	R53752	R28274	R27793	R68813		R67669	R76783	R39261	R39262	R76782	R71968	R67671	R27504	R66503	R67670	R48629	R53745
418 7	380 10	428 7	400 14			398 14			400 13					397 13	398 13		358 6		372 12		380 13	380 14	369 7	369 7		367 13		369 5		372 13	~	358 10
8.8	8.7	8.7	9.	8.5	8.5	8.5	8.5	8.5	8.5	8,3	8.2	8.2	8.2	8.2	8.2	_	_	8.1	8.1	.1	8.1	8.1	7.7	7.7	7.7	7.6				7.6	7.6	7.5
315	314	311	308	306	305	306	305	305	305	297	596	294	294	293	293	291	292	292	292	291	291	291	211	275	275	273	273	273	272	272	272	270
13	14	15	16	11	18	19	20	21	22	23	24	52	56	27	28	. 29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALI GNMENTS

amplification.		
receptor;		
RESULT 1 1D R53751 standard; Protein; 377 AA. AC R53751; DT 07-FEB-1995 (first entry) DE Seven transmembrane receptor (R2). MR Primer; seven transmembrane receptor; receptor; amplification. SHOMO sapiens.	Key Domain Albel-Transmembrane domain. Domain Domain Albel-Transmembrane domain. 11-NOV-1993; UIII53.	(ICOS-) ICOS CORP.
RESI ID AC DT DE KW	8	ΡA

Gray PW, Schweickart VL;

WPI; 94-200264/24.

Godiska R,

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sequence termed RM3. Specific primers for the partial RM3 clone were used to identify a full length RM3 cDNA clone (Q66179) which Bluescript SK-. Of sixteen clones sequenced, two contained a unique 27 ifvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 Primer; seven transmembrane receptor; receptor; amplification; PCR; Score 355; DB 9; Length 359; Pred. No. 9.41e-21; 146 kvtciiiwllaglaslpaiihrnvffientnitvcafhy 184 Gray PW, Schweickart VL; of 180-200 base pairs was observed. Seven transmembrane receptor (RM3). Location/Qualifiers Jr 3 R53753 standard; Protein; 337 AA. 'label= Transmembrane domain. /label= Transmembrane domain. Domain 287..311 /label= Transmembrane domain Match 9.9%; Local Similarity 34.0%; es 54; Conservative 07-FEB-1995 (first entry) polymerase chain reaction. 198..220 involving the receptors. 115..136 159..179 17-NOV-1993; U11153. 17-NOV-1992; US-977452. 82..100 48..69 WPI; 94-200264/24. (ICOS-) ICOS CORP. N-PSDB; Q66179. domo sapiens. MO9412635-A 09-JUN-1994 Godiska R, Query Match R53753; Domain Oomain Domain Omain))omain Omain Matches g g g П à à ð 5; 44 llaiillsvalavglpgnsfvvwsilkrmqkrsvtalmvlnlaladlavlltapfflhfl 103 104 a-qgtwsfglagcrlchyvcgvsmyasvllitamsldrslavarpfvsqklrtkamarrv 162 24 ILSMVILSLTFLLGLPGNGLVLWVAGIKMQ-RTVNTIWFLHLTIADLLCCLSIAFSLAHL 82 receptors. The probe was used to screen a human genomic foetal liver DNA library, and while the R20 gene could not be identified in Gaps Claim 2; Fig 1; 42pp; English.

Human Ang II type 1 receptor is useful for determining the bioactivity of angiotensin II type 1 receptor antagonists which are useful for treating hypertension. The Ang II type 1 receptor gene Example 10; Page 77-78; 100pp; English.

PCR using two primers (066174, 066175) was performed to amplify a partial sequence of the R20 seven transmembrane coding sequence which was later used as a probe for isolating the R20 genomic clone this library, several weakly hybridising clones were plaque purified, subcloned and sequenced. The two clones were designated R2 and R12 (066178). This is the sequence encoded by the R2 clone. (Q66176) from a human placenta DNA library. During the isolation prods, for use as therapeutic or diagnostic agents for conditions of the R20 gene, two weakly hybridising sequences were identified 2; Human angiotensin II type 1 receptor polypeptide - useful for DNA encoding seven trans:membrane receptors - used to develop determining human angiotensin II type 1 receptor antagonist which had significant homology to other seven transmembrane 10.9%; Score 390; DB 10; Length 377; 40.4%; Pred. No. 7.17e-24; 42; Mismatches 40; Indels Human angiotensin II typė I receptor. Angiotensin; Ang II; receptor; antagonist; hypertension. = = = = = Location/Qualifiers Fujisawa Y, Konishi H, Kuroda S; WPI; 94-000128/01. R44531 standard; Protein; 359 AA. 163 lagiwvlsfllatpvlayrtv 183 (TAKE) TAKEDA CHEM IND LTD. Best Local Similarity 40.4%; 24-JUN-1994 (first entry) 57; Conservative 187..313 involving the receptors. 07-APR-1992; JP-085445. 21-APR-1992; JP-101393. 17-FEB-1993; JP-027835 06-APR-1993; 093495 /note= "claim 1" CA2093495-A. N-PSDB; Q66177. N-PSDB; 053486 Homo sapiens. 08-0CT-1993, Sequence Query Match activity Protein Matches

RESULT

US-08-462-355-2.rag May 1 15:21 was derived from human placenta and is contained in plasmid 359 AA; pHARp116. Sequence ខ្លួ

;; 7; Gaps 51; Mismatches 47; Indels

24 ILSMV-IL-SLTFLLGLPGNGLVLWVAGIKMQ-RTWNTIWFLHLTLADLLCCL-SLAFSL 79 :: ::

86 vytameyrwpfgnylckiasasvafnlyasvflltclsidrylaivhpmksrlrrtmlva 145

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DNA encoding seven trans:membrane receptors - used to develop prods. for use as therapeutic or diagnostic agents for conditions Example 11; Page 84-85; 100pp; English.

Iwo primers (Q66148, Q66149) were used in a PCR reaction containing products were subjected to agarose gel electrophoresis a faint band Re-amplified material was human macrophage cDNA library in plasmid pRc/CMV. When the PCR digested with BamHI and HindIII and cloned into the plasmid

encoded this seven transmembrane receptor.

337 AA;

Sequence

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14-SEP-1992; U07641. 13-SEP-1991; US-759568. 01-APR-1993. WO9306229-A. W09217497-A. 15-0CT-1992 Sequence Query Match Matches RESULT
11D R3
AC R3
DT 26
DE Hu
KW In
KW in
OS Ho
PN WO
PP 114 RESULT
RE 셤 ð g ð 염 ð 2; 5, 83 -av-anwyfgnflckavhviytvmlyssvlilafisldrylaivhatnsgrprkllaekv 140 98 -av-anwyfgnflckavhviytvnlyssvlilafisldrylaivhatnsgrprkllaekv 155 82 LALQGQWPYGRFLCKLIPSIIVIANMFGSVFLLTAISLDRCLVVFKPIWCQNHRNVGMACS 141 33 VILSAVILSLYFLLGLDGNGLVLAVAGG-KAQRTVNTIWFLHLTLADLLCCLSLAFSLAH 81 24 iflp-tiysiifltgivgnglvilvmgyqkklrsmtdkyrlhlsvadllfvitlpfwavd 82 Gaps Gaps 23 VILSMVILSLTFLLGLPGNGLVLWVAGL-KMQRTVNTIWFLHLTLADLLCCLSLAFSLAH 81 39 iflp-tiysiifltgivgnglvilvmgyqkklrsmtdkyrlhlsvadllfvitlpfwavd 97 Disclosure; Page 54-56; 83pp; English.

2 PF4AR members were identified by probing lambda libraries from human monoclyte-like cell line HL-60 and human peripheral blood lymphocytes using a large fragment of IL-8 receptor DNA (full sequence given in Q80520). The nucleotide sequences of the 2 PF4ARs are given in Q80521 and Q80522, and their respective amino acid sequences in R68812 and R68813. inflammation; inflammatory disease; arthritis; emphysema; cystic; 5: 5; platelet factor superfamily receptor; monocyte; chemotactic; antibody capable of binding a platelet factor 4 superfamily Length 337; 9.5%; Score 340; DB 12; Length 352; 34.2%; Pred. No. 2.00e-19; 42; Mismatches 55; Indels Treatment of inflammatory disorders - by administering an 42; Mismatches 55; Indels fibrosis; colitis; bronchitis; meningitis; therapeutic. Score 340; DB 10; Pred. No. 2.00e-19; Interleukin-8 receptor; IL-8 receptor; PF4AR; 156 vyvgvwipallltipdfifanvseaddryicd-rf 189 141 vyvgvwipallltipdfifanvseaddryicd-rf 174 Chuntharapai A, Hebert C, Kim KJ, Lee J; WPI; 95-036114/05. <u>::</u> :: R68812 standard; Protein; 352 AA. Query Match 9.5%; Best Local Similarity 34.2%; Best Local Similarity 34.2%; 53; Conservative 53; Conservative 18-JUL-1995 (first entry) 22-DEC-1994. 07-JUN-1994; U06380. 11-JUN-1993; US-076093. (GETH) GENENTECH INC. Human monocyte PF4AR. receptor polypeptide N-PSDB; 080521. Homo sapiens. WO9428931-A. Sequence Query Match Matches Matches

RESULT RE

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98 -av-anwyfgnflckavhviytvnlyssvlilafisldrylaivhatnsgrprkllaekv 155 82 LALQGQWPYGRFLCKLIPSIIVLNMFGSVFLLFAISLDRCLVVFKPIWCQNHRNVGMACS 141 Gaps 39 iflp-tiysiifltgivgnglvilvmgyqkklrsmtdkyrlhlsvadllfvitlpfwavd 97 33 VILSAVILSLFFLIGLPGNGLVLAVAVAGL-KMQRTVNTIWFLHLTIADLLCCLSLAFSLAH 81 combined clone Brr.20.15 and is predicted to encode an amino acid sequence which is 34% identical with both the high and low affinity Claim 7; Fig 4; 78pp; English.

The IL-8 receptor cDNA sequence was isolated (see Q29505) and a 874bp sub-fragment of the coding sequence was used as a probe to screen human cell lime HL60 and human peripheral blood lymphocyte cDNA libraries. Two new gene sequences were found that are clearly related to the IL-8 receptor. One of these was contained in Isolated human platelet factor 4 super-family receptor polypeptide and corresp. antibodies and DNA - useful as diagnostic and screening agents, and for treating inflammation or PF4AR-mediated disorders Human II-8 receptor from clone p2.
Interleukin-8 receptor; probes; gene therapy; gro receptor; intracellula-calcium mobilising; ligand-binding; MIP-2 receptor. II-8R; G-protein coupled receptor family; rhodopsin superfamily; 2; Score 340; DB 5; Length 352; Pred. No. 2.00e-19; 42; Mismatches 55; Indels New platelet factor 4 receptor superfamily member PF4ARi. 156 vyvgvwipallltipdfifanvseaddryicd-rf 189 pro-inflammatory cytokine; Brr.20.15. R27792 standard; Protein; 352 AA. R33420 standard; Protein; 355 AA. IL-8 receptors. See also Q37107. 9.58 Best Local Similarity 34.2%; 12-MAR-1993 (first entry) Holmes WE, Lee J, Wood WI; 26-JUL-1993 (first entry) 53; Conservative 23-MAR-1992; U02317. 29-MAR-1991; US-677211. 19-DEC-1991; US-810782. (GETH) GENENTECH INC. WPI; 92-366191/44. 352 AA; N-PSDB; Q29506. Homo sapiens. Homo sapiens.

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; 106 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltqkry-lvkficls 163 86 GOMPYGRFLCKLIPSIIVLNMFGSVFLLTAISLDRCLVVFKPIMCQNHRNVGMACSICGC 145 47 viiyalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladllfaltlpiwaas-kvm 105 27 MVILSLTFLLGLPGNGLVLWVAGL-KMQRTVNTIWFLHLTIADLLCCLSIAFSLAHLALQ 85 expressed in Xenopus laevis occytes or transfected host cells, for screening ligands of IL-8 receptor and gene therapy Claim 1; Fig 3; 39pp; English. cDNA libraries from 2 and 3.5 kb fractions of poly(A) + RNA from HL60 Gaps libraries were screened with F3R oligonucleotide probe (from rabbit IL-8 receptor) and under low stringency with a p2 cDNA probe synthesised from random primers, to isolated the clone p2, encoding portions of the p2 clone as probes. P2 may also be used to screen for ligands of IL-8R and may also be used in gene therapy to treat patient deficient in IL-8R. The IL-8R is a gro receptor and has intracellular calcium-mobilising and ligand-binding properties. Sequence 355 AA; Recombinant mammalian interleukin-8 receptor - used for screening neutrophils sepd. of a sucrose gradient were made in UniZAP. The - and corresp. cDNA Disclosure; Fig 2; Tipp; English.
Rabbit high affinity IL-8 receptor gene was isolated from rabbit peritoneal neutrophils and used as a source of poly(A) + RNA, to produce a rabbit neutrophil cDNA library. 250,000 recombinant plaques were screened for those which hybridized to an antisense human IL-8 receptor protein. The presence or absence of the DNA <u>:</u> interleukin-8 binding antagonists, used to treat inflammation ecoding IL-8R or related MIP-2 receptor may be detected using Sequence in a low affinity recombinant human interleukin-8 9.3%; Score 335; DB 7; Length 355; 32.0%; Pred. No. 5.53e-19; 49; Mismatches 47; Indels IL-8 receptor polypeptide; G-protein-coupled receptor. New interleukin-8 receptor aminoacid sequence 164 iwglslllalpvllfrrtvyssnvspac-y 192 146 IWVVAFVLCIPVFVYR-EIFTTDNHNRCGY 174 (USSH) US DEPT HEALTH & HUMAN SERVICE (IL-8) receptor polypeptide in 4AB R28273 standard; Protein; 360 AA. Navarro J, Thomas KM, Witt DP; Best Local Similarity 32.0%; 48; Conservative (first entry) 10-APR-1991; US-685101. 09-JUL-1991; US-726606. 09-DEC-1991; US-803842 (REPK) REPLIGEN CORP. 10-APR-1992; U02977. (UYBO-) UNIV BOSTON WPI; 92-382123/46. 93-117549/14. N-PSDB; Q30012. N-PSDB; 038747 Homo sapiens. 04-APR-1993 W09218641-A. 29-0CT-1992. Murphy PM; Query Match R28273; Matches RESULT 쇰 ð g ð 셤 ð

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Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A. Chimeric Homo sapiens. 9 hindrance prevents the cytokines binding to a receptor in another cell. cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor harmlessly to the RBC without deleterious effect. The RBC protects the type 2 and glycophorin binding protein (GBP) 130. The use of cytokine receptors not normally found on RBCs means that the cytokine can bind 52 viiyalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladllfaltlpiwaas-kvn 110 111 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltgkry-lvkficls 168 Example A; Page 80-82; 93pp; English. Hybrid peptides for binding cytokines, comprising a malaria parasite Gaps The insert of one of these plaques, termed F3R was of 2.5 peripheral blood leukocyte lambda gtll cDNA library (5' stretch) was screened with a 652 bp EcoRI/BamHI fragment (including nucleotides 27 MVILSLIFFLIGLPGNGLVLWVAGL-KMQRTVNTIWFLHLTLADLLCCLSLAFSLAHLALQ 85 sequence derived from the second transmembrane domain of G-protein-(Plasmodium falciparum) peptide (capable of binding to a red blood nybrid peptides from excretion from the kidney, and due to steric kb in size. This insert was sequenced. The protein deduced from malaria parasite peptide capable of binding a red blood cell and This probe was designed based on the . 9 -27 to 625) of the rabbit F3R clone. After tertiary screening several human clones which hybridized to the rabbit IL-8 probe were isolated. The insert of one such clone, termed 4AB was sequenced (Q30012). coupled receptors. After tertiary screening, six plaques were New hybrid peptide(s) for binding cytokine(s) - comprising a the F3R clone demonstrates that it belongs to the family of G-protein-coupled receptors. The deduced protein sequence 9.3%; Score 335; DB 6; Length 360; 32.0%; Pred. No. 5.53e-19; indicates seven putatuve transmembrane segments. A human 49; Mismatches 47; Indels 169 iwglslllalpvllfrrtvyssnvspac-y 197 146 IWVVAFVLCIPVFVYR-EIFTTDNHNRCGY 174 = :: IL8-R type 2-GBP 130 fusion protein. R70124 standard; Protein; 1064 AA. Chimeric Plasmodium falciparum 14-FEB-1996 (first entry) Best Local Similarity 32.0%; oligonucleotide (Q30015). 48; Conservative (PREN/) PRENDERGAST K F. 03-SEP-1993; GB-018350. 23-AUG-1994; GB-017021. 01-SEP-1994; G01900. a receptor peptide. 360 AA; WPI; 95-115452/15. Prendergast KF; W09506737-A 09-MAR-1995 isolated. Sequence Query Match Matches a g g ð 88888888888888888888888 ð à

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Pred. No. 1.25e-18;

30.9%;

Best Local Similarity Matches g g 염 ð ð ð GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding 9 the surface of RBCs. The hybrid poptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological receptor molecule (eg. exhibited by Plasmodium vivax). These peptides 105 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltgkry-lvkficls 162 46 viiyalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladllfaltlpiwaas-kvn 104 27 MVILSLTFLLGLPGNGLVLWVAGL-KMQRTVNTIWFLHLTLADLLCCLSLAFSLAHLALQ 85 bind to pref. glycophorin A, B and C, sialo glycoproteins, found on Gaps oligonucleotide (Q30015). This probe was designed based on the sequence derived from the second transmembrane domain of G-protein-coupled receptors. After tertiary screening, six plaques were Recombinant mammalian interleukin-8 receptor - used for screening plaques were screened for those which hybridized to an antisense Rabbit high affinity IL-8 receptor gene was isolated from rabbit peritoneal neutrophils and used as a source of poly(A) + RNA, to **!**9 produce a rabbit neutrophil cDNA library. 250,000 recombinant interleukin-8 binding antagonists, used to treat inflammation Score 335; DB 14; Length 1064; Pred. No. 5.53e-19; Sequence in a high affinity recombinant rabbit interleukin-8 49; Mismatches 47; Indels II-8 receptor polypeptide; G-protein-coupled receptor. 163 iwglslllalpvllfrrtvyssnvspac-y 191 146 IMVVAFVLCIPVFVYR-EIFTTDNHNRCGY 174 = in F3R. R28272 standard; Protein; 355 AA. Claim 2; Fig 1; 71pp; English. Thomas KM, Witt DP; (IL-8) receptor polypeptide Query Match 9.3%; Best Local Similarity 32.0%; 04-APR-1993 (first entry) 48; Conservative 29-0CT-1992, U02977, 10-APR-1992, U02977, 10-APR-1991, US-685101. 09-UL-1991, US-726606. 09-DEC-1991, US-803842. (REPK) REPLIGEN CORP. Oryctolaque cuniculus. UNIV BOSTON. Sequence 1064 AA; WPI; 92-382123/46. = = = 030011 W09218641-A. Navarro J, damage. (UYBO-) N-PSDB; Matches

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isolated. The insert of one of these plaques, termed F3R was of 2.5

This insert was sequenced. The protein deduced from

kb in size.

the F3R clone demonstrates that it belongs to the family of G-protein-coupled receptors. The deduced protein sequence

indicates seven putatuve transmembrane segments.

355 AA;

Query Match

9.2%; Score 331; DB 6; Length 355;

A cDNA library constructed from human neutrophil mRNA in the mammalian 48 vviyalvfllsllgnslvmlvilysrsnrsvtdvyllnlamadllfaltmpiw-a-vske 105 106 kgwifgtplckvvslvkevnfysgilllacisvdrylaivhatrtltgkrh-lvkficlg 164 expression vector pRK5B was transfected into COS-7 cells as pools of 2500 clones. One positive pool from the first 58 transfections was 27 MVILSLIFILGLPGNGLVLMVAGL-KMQRTVNTIWFLHLTLADLLCCLSLAFSLAHLALQ 85 Gaps Isolated human platelet factor 4 super-family receptor polypeptide and corresp. antibodies and DNA - useful as diagnostic and screening agents, and for treating inflammation or partitioned into smaller pools until a pure clone (pRK5B.il8r1.1) IL-8R; G-protein coupled receptor family; rhodopsin superfamily; 4; Indels 50; Mismatches 49; 165 iwalslilslpfflfrqvfspnnsspvcy 193 || ::::| :| |::|::|: | 146 | IMVVAFVLCIPVFVYREIFTTDNHNRCGY 174 Location/Qualifiers R27791 standard; Protein; 350 AA. Claim 7; Fig 2; 78pp; English. -----12-MAR-1993 (first entry) Holmes WE, Lee J, Wood WI; pro-inflammatory cytokine. 46; Conservative 112..133 155..174 204..226 243..264 292..312 PF4AR-mediated disorders Interleukin-8 receptor. 19-DEC-1991; US-810782. 29-MAR-1991; US-677211. 40..67 76..98 'label= transmembrane /label= transmembrane (GETH) GENENTECH INC. /label= transmembrane /label= transmembrane 'label= transmembrane /label= transmembrane 'label= transmembrane 23-MAR-1992; U02317. WPI; 92-366191/44. /note= "putative" 'note= "putative /note= "putative" 'note= "putative' 'note= "putative' /note= "putative" 'note= "putative' N-PSDB; Q29505. Homo sapiens. W09217497-A. .5-0CT-1992 Domain Domain)omain Domain)omain Jomain Domain

9 ģ 102 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltgkrh-lvkfvclg 159 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltqkrh-lvkfvclg 159 | | :| || || || GQMPYGRELCKLIPSIIVIANMFGSVFLLTAISLDRCLVVFKPIMCQNHRNVGMACSIC-G 144 43 iiayalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladdllfaltlpiwaas-kvn 101 amino acid sequence in R68811. The receptor is used to raise antibodies that neutralize the activity of PF4AR, e.g. $\rm II-8$ receptor. 43 iiayalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladllfaltlpiwaas-kvn 101 Disclosure; Page 51-54; 83pp; English. A cDNA library constructed from human neutrophil mRNA in pRK5B was transfected into COS-7 cells, and the cells were screened with 1251-27 MVILSLIFFLIGLPGNGLVLWVAGL-KMQRTVNTIWFLHLTIADLLCCLSLAFSLAHLALQ 85 Gaps Gaps shares several features with the G-protein coupled receptors of the rhodopsin superfamily, including 7 hydrophobic (transmembrane) domains. The IL-8 receptor is a preferred PF4AR superfamily member of the invention. See also Q29506 and Q37107. encoding human IL-8 receptor, is given in 080520 and the predicted inflammation; inflammatory disease; arthritis; emphysema; cystic; was obtained. The ORF encodes a protein of 350 amino acids which platelet factor superfamily receptor; neutrophil; chemotactic; ·: ; 9 IL-8. The DNA sequence of isolated cDNA clone pRK5B.il8rl.1, antibody capable of binding a platelet factor 4 superfamily Length 350; 9.1%; Score 325; DB 5; Length 350; N.3%; Pred. No. 4.21e-18; 46; Mismatches 51; Indels Treatment of inflammatory disorders - by administering an 46; Mismatches 51; Indels fibrosis; colitis; bronchitis; meningitis; therapeutic. ==:::: Score 325; DB 12; Pred. No. 4.21e-18; Interleukin-8 receptor; IL-8 receptor; PF4AR; Lee J; c-wglsmnlslpfflfrqayhpnnsspvcy 188 | | :: | :| |::|: | : | 1 | 1.145 CIWVVAEVLCIPVEVYREIFTTDNHNRCGY 174 Chuntharapai A, Hebert C, Kim KJ, R68811 standard; Protein; 350 AA. Query Match 9.1%; Best Local Similarity 31.3%; Best Local Similarity 31.3%; (first entry) 47; Conservative 47; Conservative Interleukin-8 receptor. 11-JUN-1993; US-076093. (GETH) GENENTECH INC. 22-DEC-1994. 07-JUN-1994; U06380. receptor polypeptide WPI; 95-036114/05. 350 AA; N-PSDB; Q80520 Homo sapiens. 18-JUL-1995 W09428931-A. Sequence Sequence Query Match Matches 102 160 Matches 셤 g 5 ន្តន្តន្តន្ត 셤 유 à 8 g ð

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GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor melecule (eg. exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological ؤ Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A. Example A: Page 79-80; 93pp; English.

Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding to a red blood cell (BRC)) and a receptor peptide are claimed. R70103-25 are examples of these hybrid peptides. R0123 is a fusion of interleukin 8 receptor type I and glycophorin binding protein (GBP) 130. The use of cytokine hindrance prevents the cytokines binding to a receptor in another cell. harmlessly to the RBC without deleterious effect. The RBC protects the 102 g-wifgtflckvvsllkevnfysgilllacisvdrylaivhatrtltgkrh-lvkfvclg 159 receptors not normally found on RBCs means that the cytokine can bind 43 iiayalvfllsllgnslvmlvilysrvgrsvtdvyllnlaladllfaltlpiwaas-kvn 101 86 GQMPYGRFLCKLIPSIIVLANMFGSVFLLTAISLDRCLVVFKPIMCQNHRAVGMACSIC-G 144 86 GOWPYGRFLCKLIPSIIVLANMFGSVFLLTAISLDRCLVVFKPIWCQNHRNVCMACSIC-G 144 Gaps hybrid peptides from excretion from the kidney, and due to steric New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and ; e Score 325; DB 14; Length 1060; Pred. No. 4.21e-18; 46; Mismatches 51; Indels 160 c-wglsmnlslpfflfrqayhpnnsspvcy 188 160 c-wglsmnlslpfflfrqayhpnnsspvcy 188 145 CIWVVAFVLCIPVFVYREIFTTDNHNRCGY 174 IL8-R type 1-GBP 130 fusion protein. R70123 standard; Protein; 1060 AA. Chimeric Plasmodium falciparum 9.18; Best Local Similarity 31.3%; 14-FEB-1996 (first entry) 47; Conservative (PREN/) PRENDERGAST K F. 23-AUG-1994; GB-017021. 03-SEP-1993; GB-018350. Chimeric Homo sapiens 01-SEP-1994; G01900. 1060 AA; a receptor peptide WPI; 95-115452/15. Prendergast KF; W09506737-A 09-MAR-1995 Sequence Query Match Matches RESULT g 셤 ð g ð 셤 δ ð ð

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5 qnal-sywpfgslmcrlvmavdginqftsifcltvmsvdrylavvhptrsarwrtapvar 161 81 HIALQGQWPYGRFLCKLIPSIIVIANWFGSVFLLTAISLDRCLVVFKPIWCQNHRNVGMAC 140 somatostatin receptors (SSTR)-1, SSTR-2 and SSTR-3. The DNA encoding these proteins was isolated from total human pancreatic islet DNA. these proteins may be used in screening assays for testing candidates 45 vliplvylvvc-vvgllgnslviyvv-lrhtaspsvtnvyilnlaladelfmlglpflaa 102 including agonists and antagonists of SSTR polypeptides. The assays may be used to discriminate candidate substances with desirable 23 VILSAVILSLTFLLGLPGNGLVLAVAGLK-MQR-TVNTIWFLHLTLADLLCCLSLAFSLA 80 The sequences given in R39259, R39261 and R39263 represent the human properties specific to SSTR polypeptides. The isolated substances may be used in a wide range of aplications eg. diagnosis of various 41; Mismatches 48; Indels 5; Gaps promoter and used to transform a host cell. The DNA sequences and useful for screening candidate somatostatin receptor agonists and These DNA sequences may be placed under the control of a suitable human tumours. Fragments of these DNA sequences may be used as probes in the isolation of other SSTR-encoding clones. Human; somatostatin; receptor; SSTR-1; SSTR-2; SSTR-3; tumour; pancreas; islet; promoter; transformation; host cell. Primer; seven transmembrane receptor; receptor; amplification. Somatostatin receptors useful for diagnosis of tumours - also Score 315; DB 7; Length 418; Pred. No. 3.18e-17; Seven transmembrane receptor (R20). Location/Qualifiers Claim 3; Page 73-74; 94pp; English. R53750 standard; Protein; 380 AA. R39263 standard; Protein; 418 AA. 162 tvsaavwvasavvvlpvvvfsgv 184 Human somatostatin receptor-3. Domain 28..54 /label= Transmembrane domain. Bell GI, Seino S, Yamada Y; WPI; 93-227272/28. /label= Transmembrane domain. Query Match 8.8%; Best Local Similarity 34.3%; 07-FEB-1995 (first entry) 49; Conservative 18-NOV-1993 (first entry) 30-DEC-1992; U11327. 31-DEC-1991; US-816283. (ARCH-) ARCH DEV CORP. 96..99 N-PSDB; 045657. Homo sapiens. Homo sapiens. W09313130-A. 08-JUL-1993. antagonists Sequence R53750; R39263; Domain 103 Matches RESULT
1D R5
AC R5
DT 07
DE Se
KW Pr
COS HC
FH KE
FT DC
FT 7/1 RESULT g g පු ð ð ð

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83 plwatytyrdydwpfgtffcklssylifvnmyasvfcltglsfdrylaivrpvanarlrl 142 24 wkssgalipaiym-lvfllgttgnglvlwtvfrssrekrrsadifiaslavadltfvvtl 82 18 WNEPPVILSMVILSLTFLLGLPGNGLVLM-V-AGIKMQRTVNTIWFLHLTLADLLCCLSL 75 Gaps which was later used as a probe for isolating the R20 genomic clone (Q66176) from a human placenta DNA library. The genomic clone useful for screening candidate somatostatin receptor agonists and Example 9; Page 74-75; 100pp; English. PCR using two primers (Q66174, Q66175) was performed to amplify a partial sequence of the R20 seven transmembrane coding sequence DNA encoding seven trans:membrane receptors - used to develop prods. for use as therapeutic or diagnostic agents for conditions 39; Mismatches 51; Indels 5; Mouse; somatostatin; receptor; SSTR-1; SSTR-2; SSTR-3; tumour; Somatostatin receptors useful for diagnosis of tumours - also Score 314; DB 10; Length 380; Pred. No. 3.89e-17; pancreas; islet; promoter; transformation; host cell. Mus musculus. encodes this seven transmembrane receptor. Gray PW, Schweickart VL; 143 rvsgavat-avlwvlaallampvmvlr 168 R39264 standard; Protein; 428 AA. Murine somatostatin receptor-3. Yamada Y; 107..125 Transmembrane domain. 146..167 /label= Transmembrane domain. 'label= Transmembrane domain. label= Transmembrane domain. 'label= Transmembrane domain. Query Match 8.7%; Best Local Similarity 35.4%; Matches 52; Conservative 18-NOV-1993 (first entry) = 208..232 246..267 285..312 involving the receptors. 09-JUN-1994. 17-NOV-1993; U11153. 17-NOV-1992; US-977452. 31-DEC-1991; US-816283. (ARCH-) ARCH DEV CORP. 30-DEC-1992; U11327. Bell GI, Seino S, WPI; 93-227272/28. WPI; 94-200264/24. (ICOS-) ICOS CORP. N-PSDB; Q53750. N-PSDB; Q45658 W09313130-A. 08-JUL-1993. W09412635-A. Godiska R, Sequence Domain /label= R39264; Jomain **Jomain** Domain Domain. 쇰 ð 셤 ð 음 ð

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The sequences given in R39260, R39262 and R39264 represent the murine somatostatin receptors (SSTR)-1, SSTR-2 and SSTR-3. The DNA encoding these proteins was isolated from total murine pancreatic islet DNA. These DNA sequences may be placed under the control of a suitable promoter and used to transform a host cell. The DNA sequences and these proteins may be used in screening assays for testing candidates including agonists and antagonists of SSTR polypeptides. The assays may be used to discriminate candidate substances with desirable properties specific to SSTR polypeptides. The isolated substances may be used in a wide range of aplications eq. diagnosis of various human tumours. Fragments of these DNA sequences may be used as probes in the isolation of other SSTR-encoding clones. Sequence 428 AA;

41; Mismatches 48; Indels 5; Gaps Query Match 8.7%; Score 311; DB 7; Length 428; Best Local Similarity 34.3%; Pred. No. 7.12e-17; Matches 49; Conservative 41; Mismatches 48; Indels 윤

33 VILSMVILSLFFLEGLPGNGLVIAVAGIK-MQR-TVNTIWFLHLTLADLLCCLSLAFSLA 80 ð

104 qnal-sywpfgslmcrlvmavdginqftsifcltvmsvdrylavvhptrsarwrtapvar 162

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163 tvsravwvasavvvlpvvvfsgv 185 :: :|| :| :|| :: || :: || 141 SICGCIWVVAFVLCIPVFVYREI 163

Search completed: Wed May 1 15:29:13 1996 Job time : 58 secs.

2

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antagonists

46 ilisluyluvc-uvgllgnsluiyuv-1rhtsspsutsuyilnlaladelfmlglpflaa 103

81 HIALQCQMPYGRFLCKLIPSIIVIAMFGSVFLLTAISLDRCLVVFKPIMCQNHRAVGMAC 140

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 1 15:31:03 1996, MasPar time 11.89 Seconds 621.783 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-462-355-2 (1-482) from US08462355.pep 3591 Title:

1 MASFSAETNSTDLLSQPWNE.....TRSTHCPSNNVISERNSTTV 482 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

43470 seqs, 15335248 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 50.162; Variance 95.878; scale 0.523

Statistics:

SUMMARIES

Pred. No.	4.27e-95	1.03e - 90	1.67e-90	1.63e - 85	4.24e-85	1.41e - 81	2.64e - 79	7.35e-78	4.50e-52	1.05e-47	1.65e - 47	2.44e-45	2.44e-45
Description	C5A ANAPHYLATOXIN CHE	C5A ANAPHYLATOXIN CHE	FMLP-RELATED RECEPTOR	C5A ANAPHYLATOXIN CHE	FMLP-RELATED RECEPTOR	FMET-LEU-PHE RECEPTOR	FMET-LEU-PHE RECEPTOR	FMET-LEU-PHE RECEPTOR	TYPE-1 ANGIOTENSIN II	TYPE-1-LIKE ANGIOTENS	TYPE-1-LIKE ANGIOTENS	TYPE-1A ANGIOTENSIN I	TYPE-1 ANGIOTENSIN II
Q1	C5AR CANFA	CSAR HUMAN	FML2 HUMAN	C5AR MOUSE	FML1 HUMAN	FMLR MOUSE	FMLR RABIT	FMLR HUMAN	AG2R MELGA	AG2R_XENLA	AG2S XENLA	AG2R HUMAN	AG2R_PIG
98	-	-	æ	-	m	m	m	က	-	_	-		-
% Query Match Length DB	352	350	351	347	353	364	352	350	329	362	363	359	359
% Query Match	16.7	16.2	16.1	15.5	15.4	14.9	14.6	14.4	10.9	10.3	10.2	6.6	6.6
Score	601	580	579	555	553	536	525	518	391	369	368	357	357
Result No.	1	2	m	4	5	9	7	œ	6	10	Π	12	13

3.84e-45		3.51e-43	5.23e-42	1.28e-41	1.28e - 41	4.93e - 41	1.89e - 40	2.96e - 40	4.32e-39	3.69e - 37	5.75e-37	1.40e - 36	2.17e - 36	8.19e - 36	8.19e - 36	1.98e - 35	2.50e-33	3.87e - 33	3.87e - 33	3.87e - 33	3.87e - 33	1.61e - 33	9.29e - 33	1.44e - 32	1.44e - 32	2.23e-32	1.44e - 32	3.45e-32	8.25e-32	3.05e-31
TYPE-1 ANGIOTENSIN II	TYPE-1 ANGIOTENSIN II	TYPE-1B ANGIOTENSIN I	PROBABLE G PROTEIN-CO	TYPE-1A ANGIOTENSIN I	TYPE-1A ANGIOTENSIN I	HIGH AFFINITY INTERLE	PROBABLE G PROTEIN-CO	HIGH AFFINITY INTERLE	HIGH AFFINITY INTERLE	SOMATOSTATIN RECEPTOR	PROBABLE G PROTEIN-CO	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	MU-TYPE OPIOID RECEPT	MU-TYPE OPIOID RECEPT	HIGH AFFINITY INTERLE	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	TACHYKININ-LIKE PEPTI		KAPPA-TYPE OPIOID REC	KAPPA-TYPE OPIOID REC	SOMATOSTATIN RECEPTOR	SOMATOSTATIN RECEPTOR	OPIOID	KAPPA-TYPE OPIOID REC	SOMATOSTATIN RECEPTOR
AG2R BOVIN	AG2R_RABIT	AG2S MOUSE	LCR1 HUMAN	AG2R MOUSE	AG2R_RAT	IL8B HUMAN	LCR1_BOVIN	IL8A RABIT	IL8A HUMAN	SSR3_HUMAN	APJ HUMAN	SSR3 RAT	SSR3 MOUSE	SSR5 RAT	OPRM HUMAN	OPRM RAT	IL8B RABIT	SSR5 HUMAN	SSR1 RAT	SSR1 MOUSE	SSR1 HUMAN	TLR1 DROME	BLR1 HUMAN	OPRK_RAT	OPRK MOUSE	SSR4 RAT	SSR4 HUMAN	OPRK HUMAN	OPRK CAVPO	SSR2_BOVIN
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359	359	359	352	359	359	355	353	355	350	418	380	428	428	363	400	398	358	364	391	391	391	504	372	380	380	384	388	380	380	368
6.0 6.0	7.6	9.6	9.5	9.4	9.4	9.3	9.5	9.5	9.1	æ æ	8.7	8.7	8.7	9.8	9.8	8.5	8.2	8.2	8.3	8.2	8.2	8.2	8.1	8.1	8.1	8.1	8.1	8.0	8.0	7.9
356	350	346	340	338	338	335	332	331	325	315	314	312	311	308	308	306	295	294	294	294	294	596	292	291	291	290	291	289	287	284
14	16	11	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALI GNMENTS

								IAMMALIA;							-!- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE	ANAPHYLATOXIN C5. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE			-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.						N;		
	نہ				Œ)	1-R).		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					ER M.;		AND INFLAMM	ATES CHEMOTA	DUCTION.	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	ROTEIN COUPL						G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;		EXTRACELLULAR (POTENTIAL).
	; 352 AA.			01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)	TION UPDAT	25A ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (C5A-R).		TEBRATA;					PERRET J.J., RASPE E., VASSART G., PARMENTIER M.;		EMOTACTIC	OR STIMULA	ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION.	L MEMBRANI	1 OF G-PI					TOR.	MEMBRANE;		ACELLULAR
	PRT;		CATED)	ST SEQUEN	ST ANNOTAL	ACTIC RECH		DATA; VER					ASSART G.,	1992).	OR THE CHI	IS RECEPTO	JPEROX I DE	: INTEGRA	TO FAMILY					PROSITE; PS00237; G PROTEIN RECEPTOR.	OR; TRANS		EXTR
	STANDARD;		26, CRI	. 26, LAS	. 26, LAS	N CHEMOTI	(DOG):	OA; CHORI	ORA.		Α.		PE E., VI	BIOCHEM. J. 288:911-917(1992).	CEPTOR FO	N C5. TH	SE AND ST	LOCATION	BELONGS ?	COMCSAM.	1357.	•	i	'; G PROTI	D RECEPTO		38
			993 (REI	.993 (REL	993 (REL	HYLATOXI	CANIS FAMILIARIS (DOG).	'A; METAZ	EUTHERIA; CARNIVORA.		SEQUENCE FROM N.A.	_	1.J., RAS	J. 288:	TION: RE	HYLATOXI	TME RELEA	ELLULAR	LARITY:	EMBL; X65860; CFCOMC5AM.	PIR; S27357; S27357.	GCRDB; GCR 0558;	GCRDB; GCR_0702;	PS00237	IN COUPLE	IS.	1
RESULT 1	C5AR CANFA	P30992;	01-JUL-1	01-JUL-1	01-JUL-1	C5A ANAP	CANIS FA	EUKARYOT	EUTHERIA	Ξ	SEQUENCE	93111969	PERRET J	BIOCHEM.	-i- FUNC	ANAP	ENZY	-!- SUBC	-!- SIMI	EMBL; X6	PIR; 527	GCRDB; C	GCRDB; C	PROSITE;	G-PROTE1	CHEMOTAXIS.	DOMAIN
RESU	1	AC	DŢ	DT	Ľ	ЭE	SO	20	၁၀	RN SN	RP	Æ	Æ	R.L	ည	ပ္ပ	ខ	ဗ	႘	DR	DR	DR	DR	DR	Σ	₹	Ŀ

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FT TRANSMEM 39 61 1 (POTENTIAL). FT DOMAIN 62 72 CYTOPLASHIC (POTENTIAL). FT TRANSMEM 73 95 2 (POTENTIAL). FT TRANSMEM 112 133 95 2 (POTENTIAL). FT DOMAIN 96 111 EXTRACELJULAR (POTENTIAL). FT TRANSMEM 112 134 CYTOPLASHIC (POTENTIAL). FT TRANSMEM 155 175 4 (POTENTIAL). FT TRANSMEM 203 228 EXTRACELJULAR (POTENTIAL). FT TRANSMEM 203 228 5 (POTENTIAL). FT TRANSMEM 245 267 6 (POTENTIAL). FT TRANSMEM 245 267 6 (POTENTIAL). FT TRANSMEM 286 284 EXTRACELJULAR (POTENTIAL). FT TOOMAIN 268 284 EXTRACELJULAR (POTENTIAL). FT TOOMAIN 306 352 CYTOPLASHIC (POTENTIAL).	Query Match 16.7%; Score 601; DB 1; Length 352; Best Local Similarity 43.3%; Pred. No. 4.27e-95; Matches 71; Conservative 53; Mismatches 40; Indels 0; Gaps 0; Db 17 atldpnifvdeslntpklsvpdmialvifvmvflygypmflvvwvtgfevrrtinaiwf 76 :::: ::: ::	IND C5AR HUMAN STANDARD; PRT; 350 AA. AC P21/30; DT 01-MAY-1991 (REL. 18, CREATED) DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE) DT 01-EB-1995 (REL. 31, LAST ANNOTATION UPDATE) DT 01-EB-1995 (REL. 31, LAST ANNOTATION UPDATE) DT 01-EB-1995 (REL. 31, LAST ANNOTATION UPDATE) CSA ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (C5A-R) (CD88). GN C5R1. OS EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; RP 1156029 RA GERRAD N.P., GERARD C.; RR 71156029 RA GERRAD N.P., GERARD C.; RR 7170RE 349:614-617(1991).	

96 ivqhhhwpfggaacsilpslillnmyasilllatisadrfllvfkpiwcqnfrgaglawi 155 82 LALQCQMPYGRFLCKLIPSIIVLAMFGSVFLLTAISLDRCLVVFRPIMCQNHRNVGMACS 141 36 pdilalvifavvflvgvlgnalvvwvtafeakrtinaiwflnlavadflsclalpilfts 95 22 PVILSMVILSLTFILIGLPGNGLVLWVACLKMQRTVNTIWFLHLTLADLLCCLSLAFSLAH 81 Gaps EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ; 0 GERARD N.P., EDDY R.L. JR., SHOWS T.B., GERARD C.; Score 580; DB 1; Length 350; Pred. No. 1.03e-90; 45; Mismatches 30; Indels PROSITE; PS00237; G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) . CYTOPLASMIC (POTENTIAL). 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 01-JUL-1993 (REL. 26, IAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, IAST ANNOTATION UPDATE) FMLP-RELATED RECEPTOR II (FMLP-R-II). 351 AA. 4 (POTENTIAL). 188 BY SIMILARITY. 39320 MW; 691456 CN; 2 (POTENTIAL) . (POTENTIAL). 1 (POTENTIAL). PRT; 156 acavawglallltipsflyrvv 177 01-MAY-1992 (REL. 22, CREATED) 01-JUL-1993 (REL. 26, LAST SEQ 16.2%; GENOMICS 13:437-440(1992). Best Local Similarity 47.2%; 67; Conservative MIM; 113995; 11TH EDITION STANDARD; FPRL2 OR FPRH2 OR FPR2. HOMO SAPIENS (HUMAN) PIR; S13646; S13646. PIR; S30518; S30518. GCRDB; GCR 0054; -. 350 AA; [1] SEQUENCE FROM N.A. EUTHERIA; PRIMATES GCRDB; GCR 0293; 1 38 61 72 72 95 111 133 133 175 201 227 3 FML2 HUMAN P25090, 11-M2 CHEMOTAXIS. TRANSMEM TRANSMEM DOMAIN TRANSMEM Query Match 92307681 TRANSMEM CARBOHYD DISULFID SEQUENCE BAO L., TRANSMEM **TRANSMEM** TRANSMEM DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN Matches RESULT 셤 õ g δ g ò

SEQUENCE FROM N.A. TISSUE=BONE MARROW; 92380523

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HHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

    BIOL. CHEM. 267:7637-7643(1992).
    -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,

                                                                                                                                                          MURPHY P.M., OZCELIK T., KENNEY R.T., TIFFANY H.L., MCDERMOTT D.,
PEREZ H.D., HOLMES R., KELLY E., MCCLARY J., ANDREWS W.H.; GENE 118:303-304 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 579; DB 3; Length 351;
Pred. No. 1.67e-90;
                                                                             YE R.D., CAVANAGH S.L., QUEHENBERGER O., PROSSNITZ E.R., COCHRANE C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0237; G PROTEIN RECEPTOR.
G-PROTEIN COUPLED RĒCEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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                                                                                                        BIOCHEM. BIOPHYS. RES. COMMUN. 184:582-589(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 POTENTIAL.
139 S -> C (IN REF. 1).
38964 MW; 677967 CN;
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                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: IN
-!- SIMILARITY: BELONGS TO F
EMBL; M6672; HSFMLDX.
EMBL; M88107; HSFRHO.
EMBL; M84562; HSFPRIO.
EMBL; M84562; HSFPRIA.
EMBL; M84562; HSFPRIA.
EMBL; M84562; HSFPRIA.
EMBL; M84562; HSFPRIA.
EMBL; M67028 JO1258.
PIR; JO1251; JO1521.
PIR; B42099; B42090.
GCRDB; GCR O248; -.
GCRDB; GCR O348; -.
GCRDB; GCR O408; -.
GCRDB; GCR O408; -.
GCRDB; GCR O4013; -.
MIM; 136539; IITH EDITION.
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Local Similarity 46.5%;
les 72; Conservative
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                                                    TISSUE=GRANULOCYTE;
92246937
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                                       SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
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27 ilplvvlgvtfvlgvlgnglviwvagfrmtrtvtticylnlaladfsftatlpflivsma 86 ------

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1;

43; Mismatches 39; Indels 1; Gaps

Matches

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δλ	24 ILSMVILSLTFI	TCLPGNGLVL	ILSMVILSLTFLLGLPGNGLVLWVAGLKMQRTVNTIWFLHLTLADLLCCLSLAFSLAHLA 83
쇰	87 mgekwpfgwflc	klihivvdin	mgekwpfgwflcklihivvdinlfggvfligfialdreicylhpvwagnhrtvslamkvi 146
δλ	84 LQCQWPYGRFLC	KLIPSIIVLN	LOGQMPYGRFLCKLIPSIIVINMFGSVFLLTAISLDRCLVVFKPIWCQNHRNVGMACSIC 143
qa	147 vgpwilalvlt	pyflflttvt	vgpwilalvltlpvflflttvtipngdtyctfnfa 181
δ	:: : : : : 144 GCIWVVAFVLCIPVFVY	: :: PVFVYREIFT	:: : : :
RESULT	11.7 4		
a	5AR_MOUSE	STANDARD;	PRT; 347 AA.
AC		į	•
TO	01-JUL-1993 (REL.	797	(D)
ני בי			20, LAST SEMULACE OFDATE) 26 TAST ANNOTATION HODATE)
E B	C5A ANAPHYLATOXIN	CHEMOTACT	C5A ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (C5A-R).
S	c5AR.		
05	MUS MUSCULUS (MOUSE)	JSE),	CHORDARA, INDREDDARA, REMDADADA, MAMMAITA.
3 8	EULHERIA: RODENTIA.		si Ventebrataj tetrakuban
R.		i	
2 2	SEQUENCE FROM N.A.	ڼہ	
E &	GERARD C BAO L.	OROZCO O	PEARSON M KUNZ D GERARD N.P.;
RL	J. IMMUNOL. 149:2600-2606(1992)	2600-2606(1	992).
8	-!- FUNCTION: REC	CEPTOR FOR	CHEMOTACTIC AND INFLAMMATORY
ខ	ANAPHYLATOXIN C5.	N C5. THIS	THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE
ខម		SE AND SUPE	ENZIME KELEASE AND SUPEROAIDE ANION PRODUCTION. SUBCELIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
88	-!- SIMILARITY: 1	SELONGS TO	SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
E	EMBL; L05630; MMC5AGPR.	SAGPR.	•
DR	EMBL; S46665; S40	S46665 .	
DR.	GCRDB; GCR 0464;	i	
N C	GCRDB; GCR U618;	. C DBOTETN DECEDIOD	PECEPTOB
¥ 3	G-PROTEIN COUPLED	NECEPTOR;	TRECEFICA: TRANSMEMBRANE; GLYCOPROTEIN;
K.	CHEMOTAXIS.		
FT		33	EXTRACELLULAR (POTENTIAL).
F	TRANSMEM 34	26	
. t. t.	TRANSMEM 68	<u> </u>	CITUPLASMIC (POLENITAL).
E	DOMAIN 91	106	
FT	æ	128	<u>.</u>
FT		149	CYTOPLASMIC (POTENTIAL).
FF	TRANSMEM 150	170	4 (POTENTIAL).
T 4.	TRANSMEM 198	197	EAIRACELLOLAR (FOIENTIAL).
- E-	DOMATN 224	239	
F	æ	262	: ﴿
FT		279	EXTRACELLULAR (POTENTIAL).
타	æ	300	
	DOMAIN 301	347	CITOPLASMIC (POTENTIAL).
ı tı		104	
ÖS.	347	AA; 38510 MW;	
Ö	Ouerv Match	15,5%;	Score 555; DB 1; Length 347;
y an	Simil		1.63e-85;
×	Matches 70; Con	Conservative	46; Mismatches 45; Indels 2; Gaps 1;

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POTENTIAL. A -> G (IN REF. 2). T -> S (IN REF. 2). H -> D (IN REF. 2). My, 689682 CN; Ms, Score 553; DB 3; Length 353; D\$; Pred. No. 4.24e-85; ve 56; Mismatches 49; Indels 3; Gaps	<pre>tnfsiplneteevlpepaghtvlwifellvhgvtfvfgvlgnglviwvagfrmtrtvnti 62 :: </pre>	cylnlaladfsfeailpfrmvsvamrekwpfasflcklvhvmidinlfvsvylitiiald 122 : : :	rcicvlhpawagnhrtmslakrvmtglwiftivltlpnfifwttisttngdtycifnfaf 182 : : ::: : : : : : :: : RCLVVFKPIWCQNHRNVGMACSICGCIWVVAFVLCIFVFVYRE-IFTTDNHNRCGYKFGL 178	D; PRT; 364 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) (FMLP RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR)	CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,	JOL., CHEM. 268:25395-25401 (1993). JUOL. CHEM. 268:25395-25401 (1993). FUNCTION: LIGH AFFINITY RECEPPOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROFEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SUBILIBRITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	EIN RECEPTOR OR; TRANSMEN	EXTRACELULAR (POTENTIAL). (YTOPLASMIC (POTENTIAL). 2 (POTENTIAL). 2 (POTENTIAL). SXTRACELULAR (POTENTIAL). 3 (POTENTIAL). 4 (POTENTIAL). EXTRACELULIAR (POTENTIAL). 5 (POTENTIAL). 5 (POTENTIAL). 5 (POTENTIAL). 6 (POTENTIAL). 6 (POTENTIAL). EXTRACELULIAR (POTENTIAL). 6 (POTENTIAL).
98 176 94 94 94 111 211 213 338 338 3 AA; 40015 P 15,4%; arity 40.0%; Conservative	vlpepac : :: :LLSQPWN	ailpfr : LSLAFS	qnhrtmsla ::: QNHRNVGMA(cr.	~ Z	:25395 AFFIN RFUL N CEPTOF DIATEI OSITOI CATION	ORREC. G PROTEIN RECEPTOR;	35 58 69 91 108 1129 1170 237 237 253
D 98 T 94 T 211 T 338 E 353 AA; h Similarity 72; Conser	plneteev :: ETNSTD-L	aladfsfs : ; TLADLLCC	vlhpawaqn : VFKPIWCQN	(RE (RE E RE	MUSCULUS (MOUSE) RRYOTA; METAZOA; IERIA; RODENTIA. FENCE FROM N.A. 44602	JOL., NORTH F.P. 101. IOL. CHEM. 268:25395- FUNCTION: HIGH AFFINI WHICH ARE POWERFUL NE FMLP TO THE RECEPTOR RESPONSE IS MEDIATED PHOSPHATIDYLINGSITOL- SUBCELLULAR LOCATION: SIMILARITY: BELGATION:	81; MMNF 0684; - 500237; COUPLED	; 31 36 59 70 92 109 1130 171 217 238 254 278
DISULFID CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE SEQUENCE Query Match Best Local Si Matches 72	3 tnfsi :: 2 ASFSA	63 cylnl : : 60 WFLHL	123 rcicv : 120 RCLVV	MLF 1-F 1-F 1-J 1-J	MUS MUSCULUS (MOUSE EUKARYOTA; METAZOA; EUTHERIA; RODENTIA. IJ SEQUENCE FROM N.A. 94064602 GAO JI., MIRBPHY P.	J. BIOL. C -!- ENCT HICK FALLY FMLC T -!- SUBCELT -!- SIBILIA	7088	CHEWOTAXIS, DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM TRANSMEM TRANSMEM TRANSMEM DOMAIN TRANSMEM DOMAIN
FT FT SO Ou Be	DP Qy	Q y	DP Oy	RESULT ID F AC P DT 0 DT 0 DE F DE (S S S S S S S S S S S S S S S S S S S	4	MA DA	ET E

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									e; Gaps	fyiasm 93	FSLAHL 82	slakkv 153	GMACSI 142	202	195
d.	(1 kg	. /1					angth 364;		Indels	35 vfsylifavtfvlgvlgnglviwvagfrmkhtvttisylnlaiadf-cftstlpfyiasm 93	ILSMVILSLTFLIGLEPGNGLVLWVAGLKMQRTVNTIWFLHLTLADLLCCLS-LAFSLAHL 82	94 vmgghwpfgwfmckfiytvidinlfgsvflialialdarcicvlhpvwaqnhrtvslakkv 153	83 ALGCOMPYCRFLCKLIPSIIVLANFGSVFLLTAISLDRCLVVFKPINCONHRNVGMACSI 142	154 iivpwicaflltlpvii-r-l-ttvpnsrlg-pgktactfdfspwtkdpvekr 202	
2-355-2 rs	7 (POTENTIAL).					'N'	DB 3; Le	l.41e-81;	ches 38;	tisylnlais	TIWE LHLTL	ialdrcicvlh	SLDRCLWF	yktactfdfspwt	GESSSLDYPI
US-08-462-355-2 rsp	7 (POTENTIAL).	POTENTIAL.	POTENTIAL.	POTENTIAL.	POTENTIAL.	40327 MW; 733437 CN;	Score 536; DB 3; Length 364;	Pred. No. 1.41e-81;	54; Mismatches 38;	vagfrmkhtvi	VAGLKMORTV	lfgsvflial:	MFGSVFLLTA	wicaflltlpvii-r-l-ttvpnsrlg-po	TDNHNRCGYKI
	316	, A.	10	18	187	40327 MW	14.98;		rvative	yvlgnglviw	SLPGNGLVLA	cfiytvidin	LIPSIIVLA	ovii-r-l-t	VEVYREIFT
	297	4	10	18	106	364 AA;		imilarity	75; Conservative	lifavtfvld	VIESLTFLIK	hwpfgwfmcl	OWPYGRFLCE	wicaflltly	WVAFVLCII
May 1 15:23	TRANSMEM	CARBOHYD	CARBOHYD	CARBOHYD	DISULFID	SEQUENCE	Query Match	Best Local Similarity 43.4%;	Matches 7	35 vfsy	24 ILSM	94 vmgg	83 ALQG	154 iivp	143 CCCI
Mg.		F	FI	F	FT	Š	õ	æ	E	g	ò	qq	ó	qq	à

-i- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- TISSUE SPECIFICITY: NEUTROPHILS.
-!- SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
-EMBL, M94549; OCFPR. YE R.D., QUEHENBERGER O., THOMAS K.M., NAVARRO J., CAVANACH S.L., PROSSNITZ E.R., COCHRANE C.G.; 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) FMET-LEU-PHE RECEPTOR (FMLP RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR) EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; LACOMORPHA. STRAIN=NEW ZEALAND WHITE; TISSUE=NEUTROPHILS; 352 AA. PRT; J. IMMUNOL. 150:1383-1394 (1993). ORYCTOLAGUS CUNICULUS (RABBIT). 01-FEB-1994 (REL. 28, CREATED) 01-FEB-1994 (REL. 28, LAST SEQ 01-JUN-1994 (REL. 29, LAST ANN STANDARD; SEQUENCE FROM N.A. FMLR RABIT 93163563 005394; (FPR). The state of the s

RESULT

ÿ 87 lgghwpfgwflckfvftivdinlfgsvflialialdrcicvlhpvwagnhrnvslakkvi 146 24 ILSMVIISLIFELGEPRGEVEWAYAGIKMQRTVNTIWFEHLTIADLECCESLAFSLAHLA 83 27 vísylilvvtívlgvlgnglvimvtgírmthtvttisylnlaladfsítstlpífivtka 86 Gaps FMET-LEU-PHE RECEPTOR (FMLP RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR) EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ä, Score 525; DB 3; Length 352; Pred. No. 2.64e-79; 44; Mismatches 31; Indels 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL). SUBMITTED (MAR-1993) TO EMBL/GENBANK/DDBJ DATA BANKS. CYTOPLASMIC (POTENTIAL). BOULAY F., TARDIF M., BROUCHON L., VIGNAIS P.; BIOCHEM. BIOPHYS. RES. COMMUN. 168:1103-1109(1990) L., VIGNAIS P.; LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) 350 AA (POTENTIAL) . 4 POTENTIAL.
10 POTENTIAL.
178 POTENTIAL.
38674 MM; 662482 CN; (POTENTIAL) 147 vgpwicallltlpvii-r-v-ttlshpr 171 BIOL. CHEM. 266:12560-12567 (1991). PRT; BOULAY F., TARDIF M., BROUCHON L., BIOCHEMISTRY 29:11123-11133(1990) 01-MAY-1991 (REL. 18, CREATED) 01-MAY-1991 (REL. 18, LAST SEQU 01-OCT-1994 (REL. 30, LAST ANNO Query Match 14.6%; Best Local Similarity 47.3%; 91286286 MURPHY P.M., MCDERMOTT D.; 70; Conservative STANDARD; 162 207 228 244 268 287 307 352 HOMO SAPIENS (HUMAN) 352 AA; EUTHERIA; PRIMATES [1] SEQUENCE FROM N.A. 141 163 208 229 245 245 269 308 4 10 PEREZ H.D.; FMLR HUMAN DOMAIN TRANSMEM DOMAIN TRANSMEM 91105045 90267449 TRANSMEM CARBOHYD CARBOHYD DISULFID SEQUENCE DOMAIN P21462; (FPR). DOMAIN 00 FPR1. Matches [2] 임 g g ð ð ð

94040825

EXTRACELIJIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).

PROSITE, PSO0237, G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR, TRANSMEMBRANE; GLYCOPROTEIN;

CHEMOTAXIS.

DOMAIN TRANSMEM

PIR; A46520; A46520. GCRDB; GCR 0537; -. EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL).

(POTENTIAL) 2 (POTENTIAL)

27 50 61 61 83 83 120 140

28 28 51 62 62 84 84 101

PRANSMEM

DOMAIN

DOMAIN TRANSMEM DOMAIN

MURPHY P.M., TIFFANY H.L., MCDERMOTT D., AHUJA S.K.;

GENE 133:285-290(1993)

-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES

WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; M60626; HSFMLP. EMBL; M60627; HSFMLP26.

EMBL; L10820; HSFPR1A.

PIR; A35495; A35495. PIR; A36309; A36309.

PROSITE; PSO0237; G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

CHEMOTAXIS; POLYMORPHISM

TRANSMEM TRANSMEM

DOMAIN DOMAIN

GCRDB; GCR_0069; -.
GCRDB; GCR_0070; -.
GCRDB; GCR_065; -.
MIM; 136537; 11TH EDITION.

EXTRACELLULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

-!- POLYMORPHISM: THE VARIANT SEQUENCES ARE THOUGHT TO BE DUE TO

TISSUE SPECIFICITY: NEUTROPHILS.

ALLELIC VARIATION OF A SINGLE GENE.

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

DOMAIN TRANSMEM DOMAIN TRANSMEM

(POTENTIAL) .

EXTRACELLULAR (POTENTIAL) .

(POTENTIAL)

83 100 1121 140 1162 205 226 242 242 266 285 305 3305

TRANSMEM

DOMAIN DOMAIN DOMAIN DOMAIN

CYTOPLASMIC (POTENTIAL).

(POTENTIAL) (POTENTIAL).

RANSMEM **PRANSMEM** CARBOHYD

CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL).

RESULT

146 iigpwvmallltlpvii 162

g ð

86 amgghwpfgwflckflftivdinlfgsvflialialdrcvcvlhpvwtgnhrtvslakkv 145

q

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27 iitylvfavtfvlgvlgnglviwvagfrmthtvttisylnlavadf-cftstlpffmvrk 85

a ð

2;

Gaps

2;

Score 518; DB 3; Length 350; Pred. No. 7.35e-78; 46; Mismatches 25; Indels

Query Match 14.4%; Best Local Similarity 46.7%;

64; Conservative

Matches

셤

A -> E. POTENTIAL. POTENTIAL. POTENTIAL.

38401 MW;

SEQUENCE

DISULFID

CARBOHYD VARIANT VARIANT

L -> V.

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4; MELEAGRIS GALLOPAVO (COMMON TURKEY). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; 88 tameyqwpfgnclcklasagisfnlyasvflltclsidrylaivhpvksrirrtmfvarv 147 MURPHY T.J., NAKAMURA Y., TAKEUCHI K., ALEXANDER R.W.;

MOL. PHARMACOL. 44:1-7(1993).

-!— FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL—
CALCIUM SECOND MESSENGER SYSTEM. 29 imvptvysiifiigifgnslvviviycymklktvasifllnlaladl-cflitlplwaay 87 !- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED Gaps -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. 5; 10.9%; Score 391; DB 1; Length 359; 38.2%; Pred. No. 4.50e-52; 46; Mismatches 46; Indels PROSITE, P500237; G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) 359 AA. (POTENTIAL). 4 (POTENTIAL). (POTENTIAL) . (POTENTIAL). 1 (POTENTIAL) . BY SIMILARITY. 732730 CN; (POTENTIAL) (POTENTIAL) -!- TISSUE SPECIFICITY: ADRENAL MEDULLA. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. TYPE-1 ANGIOTENSIN II RECEPTOR (AT1). PRT; 41250 MW; STANDARD; (REL. 28, C (REL. 28, I (REL. 28, I 01-FEB-1994 01-FEB-1994 01-FEB-1994 AG2R MELGA δ 염 δ US-08-462-355-2.rsp

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Matches g g 8 ò

g 8

GCRDB; GCR 0763; -. PROSITE; P500237; G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN; -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA. -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. BERGSMA D.J., ELLIS C., NUTHULAGANTI P.R., NAMBI P., SCAIFE -!- TISSUE SPECIFICITY: HEART MEMBRANES, FOLLICULAR OOCYTES EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) CYTOPLASMIC (POTENTIAL) SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PALMITATE (POTENTIAL). PALMITATE (POTENTIAL). 01-JUN-1994 (REL. 29, IAST ANNOTATION UPDATE) TYPE-1-LIKE ANGIOTENSIN II RECEPTOR 2 (ATI). XENOPUS LAEVIS (AFRICAN CLAMED FROG). 363 AA. (POTENTIAL). BY SIMILARITY. (POTENTIAL). 3 (POTENTIAL). LAST SEQUENCE UPDATE) (POTENTIAL). (POTENTIAL) (POTENTIAL) 745704 CN; POTENTIAL. POTENTIAL CALCIUM SECOND MESSENGER SYSTEM PRT; KUMAR C., AIYAR N.; MOL. PHARMACOL, 44:277-284(1993). 41540 MW; (REL. 29, CREATED) (REL. 29, LAST SEQ PALMITATE; PHOSPHORYLATION. STANDARD; EMBL; U01155; XL155. 363 AA; SEQUENCE FROM N.A. 263 276 297 LISSUE=HEART; LT 11 AG2S_XENLA P35373; 01-JUN-1994 01-JUN-1994 PRANSMEM SEQUENCE **FRANSMEM FRANSMEM PRANSMEM FRANSMEM** FRANSMEM FRANSMEM CARBOHYD CARBOHYD DISULFID DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN OMAIN DOMAIN LIPID LIPID

ö 87 avytamhyhwpfgdllckiastaitlnlyttvflltclsidrysaivhpmksrirrtvmv 146 29 ifitipiiystifvvgvfgnslvviviysymkm-ktmasvflmnlalsdl-cfvitlplw 86 23 VILSH-VILSLIFILGLPGNGLVLWVA-G-LKMQRTVNTIMFLHLFLADLLC-CLSLAFS 78 Gaps 8 Score 368; DB 1; Length 363; Pred. No. 1.65e-47; 51; Mismatches 44; Indels 10.2%; 34.4%; Best Local Similarity 34.4%; Matches 54; Conservative Query Match

MIM, 106165, 11TH EDITION. PROSITE; PS00237, G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR, TRANSMEMBRANE; PALMITATE; PHOSPHORYIATION.	FT DOMAIN 1 2/1 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 53 64 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 65 87 2 (POTENTIAL). FT TRANSMEM 65 87 2 (POTENTIAL). FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 103 124 3 (POTENTIAL). FT TRANSMEM 143 162 4 (POTENTIAL). FT TRANSMEM 143 162 4 (POTENTIAL). FT TRANSMEM 143 162 6 (POTENTIAL). FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 241 262 6 (POTENTIAL). FT TRANSMEM 241 262 6 (POTENTIAL). FT TRANSMEM 276 296 7 (POTENTIAL). FT TRANSMEM 276 296 7 (POTENTIAL). FT TRANSMEM 276 296 7 (POTENTIAL). FT CARBOHYD 4 4 POTENTIAL. FT CARBOHYD 176 176 POTENTIAL. FT CARBOHYD 176 176 POTENTIAL. FT TRANSMEM 253 355 POTENTIAL.	SEQUENCE 359 AA; 41061 MM; Query Match 9.94; S Best Local Similarity 33.74; P Matches 56; Conservative 5 27 ifymiptlysiifvvqifqislavy 27 ifymiptlysiifvvqifqislavy 27 ifymiptlysiifvvqifqislavy 27 ifymiptlysiifvvqifqislavy 27 ifymiptlysiifvvqifqislavy 28 ILSMV-IL-SITFLIGIPGNGLVL	Db 86 vytameyrwpfgnylckiasasvsfiltclsidrylaivhpmksrlrrtmlva 145 ::: : : ::: ::	RESULT 13 ACT PAGE PIG STANDARD; PRT; 359 AA. AC P33555; DT 01-APR-1993 (REL. 25, CREATED) DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE) DT 01-APR-1993 (REL. 29, LAST ANNOTATION UPDATE) DE TYPE-1 ANGIOTENSIN II RECEPTOR (ATI). OS SUS SCROFA (PIG). OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; RN [1] RN SEQUENCE FROM N.A. RC 715SUB-AORTIC SMOOTH MUSCLE; RM 9355923 RA ITAZAKI K., SHIGERI Y., FUJIMOTO M.; RL OIL J. PHARAKOOL. 245:147-156 (1993). CC -! FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY CC ASSOCIATION MITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL- CC CALCIUM SECOND MESSENGER SYSTEM. CC -!- PTW: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. CC -!- PTW: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. CC -!- PTW: CARBOXYL-TERMINAL SER OR THR MESIDUES MAY BE PHOSPHORYLATED.
Db 147 arltcogiwlvaflaslpsviyrqififpdtnqtvca 183 : : : : : : : Qy 139 ACSICGCIWVVAFVLCIPVFREIFT-TD-NHNRCG 173	RESULT 12 AC P30556; DT 01-ARR-1993 (REL. 25, CREATED) DT 01-ARR-1993 (REL. 25, LAST SEQUENCE UPDATE) DT 01-ARR-1993 (REL. 29, LAST SEQUENCE UPDATE) DC 01 01-ARR-1993 (REL. 29, LAST SEQUENCE NORMAN). CA AGTRI OR AT2RI. CA AGTRI OR AT2RI. CA CRARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; CEUTHERIA; PRIMATES. RN [1] RP SEQUENCE FROM N.A. RA 92337608 RA MAUCY C.A., HRANG O., EGLOFF A.M., WU L.H., CHUNG FZ.; RL BIOCHEM. BIOPHYS. RES. COMMON. 186:277-284 (1992). RN [2] RN FEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA PSEQUENCE FROM N.A.			RM [5] RM CURNOW K.M., PASCOE L., WHITE P.C.; RA CURNOW K.M., PASCOE L., WHITE P.C.; RA CURNOW K.M., PASCOE L., WHITE P.C.; ROL. ENDOCRINOL. 6:1113-1118(1992). C!- FUNCTION! RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROFINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL—CC CALCIUM SECOND MESSENGES YSTEM. C!- TISSUE SPECIFICITY: LIVER, LUNG, ADRENAL, AND ADRENOCRTICAL ADSOMAS. C!- PTH: CARBOWAS. C!- PTH: ANGIALINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. C!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN. C!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN. C!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN. C!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROFEIN COUPLED RECEPTORS. DR EMBL; M91246; HSATIR. DR EMBL; M91344; HSATIR. DR EMBL; M93394; HSATIR. DR EMBL; M93394; HSATIR. DR GCRB; GCR 0296; DR GCRB; GCR 0384; DR GCRB; GCR 0481; DR GCRB; CCR 0471; DR GCRB; CCR 0471;

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106165; 11TH EDITION. TTETE, PROSECUST, G PROTEIN. TTATE, PHOSPHORYLATION. IN 1 27 SWEM 28 52 SWEM 103 124 SWEM 103 126 SWEM 215 240 SWEM 215 112 IN 112 IN 112 IN 112 IN 113			GLYCOPROTEIN; LIPOPROTEIN;		(POTENTIAL).		NTIAL).		(POTENTIAL).		(POTENTIAL).	•	(POTENTIAL).		(POTENTIAL).		(POTENTIAL).		(POTENTIAL).					IAL).		Length 359;		48; Indels 8; Gaps 8;	Inlaladl-cflltlplwa 85		LHLTIADLLCCL-SLAFSL 79	ylaivhpmksrlrrtmlva 145		CLVVFKP IWCQNHRNVGMA 139	qnstl 191	- :	LSSSL 182
MIM; 106165; 11TH EDITION PROSITE; PSO0237, G. PROTEI C-PROTEIN COUPLED RECEPTO DOMAIN 1 27 TRANSMEM 28 52 DOMAIN 53 64 TRANSMEM 103 124 DOMAIN 125 142 TRANSMEM 193 214 DOMAIN 163 124 DOMAIN 263 246 TRANSMEM 193 214 DOMAIN 263 247 TRANSMEM 241 262 DOMAIN 263 246 TRANSMEM 241 262 DOMAIN 263 246 TRANSMEM 241 262 DOMAIN 263 319 TRANSMEM 241 262 DOMAIN 263 319 TRANSMEM 241 262 DOMAIN 263 319 TRANSMEM 276 296 TRANSMEM 276 TRANSMEM 27	░.	IN RECEPTOR.	TRANSMEMBRANE;	×.	EXTRACELLULAR	<pre>1 (POTENTIAL).</pre>	CYTOPLASMIC (POTE)	2 (POTENTIAL).		3 (POTENTIAL).	CYTOPLASMIC (POTE	4 (POTENTIAL).		5 (POTENTIAL).				<pre>7 (POTENTIAL).</pre>		POTENTIAL.	POTENTIAL.	POTENTIAL.	BY SIMILARITY.		MM;	Score 357;	Pred. No. 2.44e-4	54; Mismatches	ıslvviviyfymklktvasvfl	:: :: -: -: :: :: :: :: :: :: :: :: :: :	IGLVLWVAGLKMQ-RTVNTIWF	asvsfnlyasvflltclsidr		SIIVLNMFGSVFLLTAISLDR	hrnvffientnitvcafhyes		YREIFTTDNHN-R-CGYKF-G
MIN, 106165 PROSITE; PS G-PROTEIN O PALMITATE, POMAIN TRANSMEM DOMAIN TRANSMEM TR		00237; G PROTE	OUPLED RECEPTO	PHOSPHORYLATION	1 27															4 4						86.6	Llarity	Conser	tlysiifvvgifgn	= :::::::::::::::::::::::::::::::::::::	IL-SLTFLLGLPGN	yrwpfgnylckias	:: ::: :::	GQWPYGRFLCKLIP	iwllaglaslpaii	:: :: :: :: ::	IWVVAFVLCIPVFV
	MIM: 106165	PROSITE; PS	G-PROTEIN CO	PALMITATE; 1	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	TRANSMEM	DOMAIN	CARBOHYD	CARBOHYD	CARBOHYD	DISULFID	LIPID	SEQUENCE	nerv Match		Matches 56;		<u>:-</u>			<u>:</u>	80 AHLALQ	146 kvtcii		140 CSICGC

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May 1 15:23

RATTUS NORVEGICUS (RAT). STRAIN-SPRAGUE-DAWLEY; LT 15 AG2S_RAT P29089; 92183879 TRANSMEM **PRANSMEM TRANSMEM** RANSMEM CARBOHYD CARBOHYD SEQUENCE DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN Matches g 쉱 g δ ð δ ä 86 vytameyrwpfgnylckiasasvsfnlyasvflltclsidrylaivhpmksrlrrtmlva 145 GCRDB; GCR 0592; -. PROSITE; P500237; G PROTEIN RECEPTOR. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN; PALMITATE; PHOSPHORYLATION. ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-Gaps SASAKI K., YAMANO Y., BARDHAN S., IWAI N., MURRAY J.J., HASEGAWA M., MATSUDA Y., INAGAMI T.; NATURE 351:230-233(1991). SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; .. 8 Score 357; DB 1; Length 359; Pred. No. 2.44e-45; 54; Mismatches 48; Indels 146 kvtciiiwllaglaslptiihrnvffientnitvcafhyesqnstl 191 EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL). CYTOPLASMIC (POTENTIAL) PALMITATE (POTENTIAL). 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) (POTENTIAL). (POTENTIAL). 4 (POTENTIAL). 359 AA. (POTENTIAL) . BY SIMILARITY (POTENTIAL) (POTENTIAL) 40906 MW; 730725 CN; POTENTIAL. POTENTIAL. POTENTIAL TYPE-1 ANGIOTENSIN II RECEPTOR (AT1). CALCIUM SECOND MESSENGER SYSTEM PRT; Query Match 9.9%; Best Local Similarity 33.7%; 56; Conservative STANDARD; EUTHERIA; ARTIODACTYLA. 188 180 355 BOS TAURUS (BOVINE). SSA2R. 188 101 355 359 AA; SEQUENCE FROM N.A. 28 53 65 88 103 1125 143 163 193 215 241 263 276 EMBL; D11340; AG2R BOVIN DOMAIN TRANSMEM TRANSMEM TRANSMEM DOMAIN TRANSMEM DISULFID SEQUENCE TRANSMEM CARBOHYD CARBOHYD 91251900 TRANSMEM TRANSMEM CARBOHYD P25104; DOMAIN DOMAIN DOMAIN DOMA IN DOMAIN DOMAIN LIPID 24 Matches RESULT

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prosite; p\$00237; c protein receptor. G-protein coupled receptor; transmembrane; glycoprotein; lipoprotein; -!- TISSUE SPECIFICITY: ADRENAL MEDULLA, CORTEX, AND KIDNEY.
 -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. EXTRACELLULAR (POTENTIAL) c vecientiam .
EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) . 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) . BY SIMILARITY.
PALMITATE (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL) (POTENTIAL) 4 (POTENTIAL) (POTENTIAL) 724453 CN; POTENTIAL. POTENTIAL. POTENTIAL. . E PALMITATE; PHOSPHORYLATION. 41088 EMBL; X62294; BTAAIITIR. PIR; S15403; S15403. 27 52 64 1102 1124 1162 216 2216 2216 2216 359 4 176 188 180 355 359 AA; GCRDB; GCR 0372; 28 53 65 65 88 103 125 143 163 193 215 CARBOHYD DISULFID DOMAIN TRANSMEM DOMAIN TRANSMEM TRANSMEM

ö 86 vytameyrwpfgnylckiasasvsfnlyasvflltclsidrylaivhpmksrlrrtmlva 145 27 ifimiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 Gaps .. 80 Query Match 9.9%; Score 356; DB 1; Length 359; Best Local Similarity 33.7%; Pred. No. 3.84e-45; 54; Mismatches 48; Indels 146 kvtciiiwllaglaslptiihrnvffientnitvcafhyesqnstl 191 56; Conservative

01-DEC-1992 (REL. 24, CREATED) 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) 359 AA. TYPE-1B ANGIOTENSIN II RECEPTOR (AT1B) (AT3) PRT; STANDARD;

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. SEQUENCE FROM N.A.

IWAI N., INAGAMI T.;

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May 1 15:23

-!- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE FRUIELIN.
-!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
-!- TISSUE SPECIFICITY: IS EXPRESSED IN THE LIVER, KIDNEY, AORTH, LUNG, UTERUS, OVARY, SPLEEN, HEART, ADRENAL GLAND, AND VASCULAR SMOOTH MUSCLE CELL.
-!- SIMILARIY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-ELTON T.S., STEPHAN C.C., TAYLOR G.R., KIMBALL M.G., MARTIN M.M., DURAND J.N., OPARIL S.; BIOCHEM. BIOPHYS. RES. COMMUN. 184:1067-1073(1992). KAKAR S.S., SELLERS J.C., DEVOR D.C., MUSCROVE L.C., NEILL J.D.; BIOCHEM. BIOPHYS. RES. COMMUN. 183:1090-1096(1992). PIR; A42656; A42656.
PIR; S20423; S20423.
PIR; JH0578; JH0578.
PIR; J0516; J0516.
GCRDB; GCR 0245; -GCRDB; GCR 0378; -GCRDB; GCR 0422; -GCRD -> I (IN REF. 3 AND 4). -> M (IN REF. 3 AND 4). -> Y (IN REF. 4). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) SANDBERG K., JI H., CLARK A.J., SHAPIRA H., CATT K.J.; EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). (POTENTIAL). (POTENTIAL). BY SIMILARITY. 3 (POTENTIAL). (POTENTIAL) . (POTENTIAL) POTENTIAL. POTENTIAL. POTENTIAL. CALCIUM SECOND MESSENGER SYSTEM. J. BIOL. CHEM. 267:9455-9458 (1992) FEBS LETT. 298:257-260(1992). SEQUENCE FROM N.A. TISSUE=ANTERIOR PITUITARY; [2] SEQUENCE FROM N.A. TISSUE=ADRENAL CORTEX; -!- SIMILARITY: BELONGS EMBL; X64052; RRATIBG. EMBL; M90065; RRAGTIIR. 27 52 64 87 87 1124 1124 1162 1162 2140 2240 2275 2275 2275 2376 2359 4 176 188 180 40 EMBL; M87003; RNANGII. SEQUENCE FROM N.A. PHOSPHORYLATION.
DOMAIN
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TRANSMEM
28 215 241 263 276 297 DOMAIN TRANSMEM DOMAIN CARBOHYD DOMAIN TRANSMEM CONFLICT DOMAIN TRANSMEM DOMAIN TRANSMEM 92250585 92231868 CARBOHYD CARBOHYD DISULFID 92246922 **PRANSMEM PRANSMEM** CONFLICT DOMAIN DOMAIN

40911 MW; 719418 CN; 359 AA; SEQUENCE g

ö 53; Mismatches 49; Indels 8; Gaps Length 359; Score 352; DB 1; Pred. No. 2.34e-44; Query Match 9.8%; Best Local Similarity 33.7%; Matches 56; Conservative

27 ifvmiptlysiifvvgifgnslvviviyfymklktvasvfllnlaladl-cflltlplwa 85 g ð

86 vytameyrwpfgnhlckiasasvsfnlyasvflltclsidrylaivhpmksrlrrtmlva 145 g

|:::||:| ||:::||:| ||::::||:||||||| ||:||| ||:|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||

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